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(21) International Application Number: PCT/US95/12463 (22) International Filing Date: 27 September 1995 (27.09.95) (30) Priority Data: 08/315,961 30 September 1994 (30.09.94) US (71) Applicant: LUDWIG INSTITUTE FOR CANCER RE- SEARCH [CH/US]; 1345 Avenue of the Americas, New York, NY 10105 (US). (72) Inventors: VAN DER BRUGGEN, Pierre; UCL 7459, Avenue Hippocrate 74, B-1200 Brussels (BE). BOON-FALLEUR, Thierry; UCL 7459, Avenue Hippocrate 74, B-1200 Brussels (BE). VAN DEN EYNDE, Benoit; UCL 7459, Avenue Hippocrate 74, B-1200 Brussels (BE). (74) Agent: HANSON, Norman, D.; Felfe & Lynch, 805 Third Avenue, New York, NY 10022 (US).		(81) Designated States: AU, CA, CN, FI, JP, NO, NZ, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
(54) Title: COMPOSITIONS CONTAINING TUMOR REJECTION ANTIGEN PRECURSORS OR TUMOR REJECTION ANTIGENS, AND AN ADJUVANT AND/OR GROWTH FACTOR (57) Abstract Compositions with improved immunogenic effect are disclosed. The compositions contain one or more peptides which, when complexed with a cell surface molecule, such as an MHC, HLA or B cell receptor, provoke an immune response. The compositions contain adjuvants such as saponins, which potentiate the immune response. Especially preferred are compositions which stimulate cytolytic T cell responses, such as peptides which satisfy criteria for MHC binding, such as peptides derived from tumor rejection antigen precursors, including MAGE, BAGE, and GAGE derived peptides.		

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COMPOSITIONS CONTAINING TUMOR REJECTION ANTIGEN
PRECURSORS OR TUMOR REJECTION ANTIGENS,
AND AN ADJUVANT AND/OR GROWTH FACTOR

RELATED APPLICATIONS

This application is a continuation in part of all of the following applications, each of which discuss the provocation of cytolytic T cells in the presence of complexing tumor rejection antigens and MHC/HLA molecules: PCT application PCT/US92/04354 (designating the United States); Serial No. 938,334, filed August 31, 1992; Serial No. 008,446, filed January 22, 1993; Serial No. 54,714, filed April 28, 1993; Serial No. 203,054, filed February 28, 1994; Serial No. 233,305, filed April 26, 1994; Serial No. 195,186, filed February 14, 1994; Serial No. 196,630, filed February 15, 1994; Serial No. 32,978, filed March 18, 1993; Serial Nos. 217,186; 217,187; and 217,188, all of which were filed on March 24, 1994; Serial No. 190,411, filed on April 1, 1994 and Serial No. 253,503, filed June 3, 1994.

FIELD OF THE INVENTION

This invention relates to compositions useful in the generation of an immune response against the classes of molecules referred to as tumor rejection antigen precursors ("TRAPs") and tumor rejection antigens ("TRAS"). The immune response includes, inter alia, the production of antibodies against the TRAPs and TRAS, as well as T cells specific for complexes of TRA and major histocompatibility molecules ("MHCs"). Such T cells and antibodies may be generated, e.g., in a mouse, rat, rabbit, sheep, goat or other non-human animal, and then used in diagnostic methods to identify tumor presence. The compositions may also be used, therapeutically, via administration to a subject afflicted with a cancerous condition or one where cell transformation has taken place, such as melanoma or dysplastic nevi, to provoke an

5 immune response against tumors, cancer cells, and transformed cells.

BACKGROUND AND PRIOR ART

10 The study of the recognition or lack of recognition of cancer cells by a host organism has proceeded in many different directions. Understanding of the field presumes some understanding of both basic immunology and oncology.

15 Early research on mouse tumors revealed that these displayed molecules which led to rejection of tumor cells when transplanted into syngeneic animals. These molecules are "recognized" by T-cells in the recipient animal, and provoke a cytolytic T-cell response with lysis of the transplanted cells. This evidence was first obtained with tumors induced in vitro by chemical carcinogens, such as methylcholanthrene.

20 The antigens expressed by the tumors and which elicited the T-cell response were found to be different for each tumor. See Prehn, et al., J. Natl. Canc. Inst. 18: 769-778 (1957); Klein et al., Cancer Res. 20: 1561-1572 (1960); Gross, Cancer Res. 3: 326-333 (1943), Basombrio, Cancer Res. 30: 2458-2462 (1970)

25 for general teachings on inducing tumors with chemical carcinogens and differences in cell surface antigens. This class of antigens has come to be known as "tumor specific transplantation antigens" or "TSTAs". Following the observation of the presentation of such antigens when induced

30 by chemical carcinogens, similar results were obtained when tumors were induced in vitro via ultraviolet radiation. See Kripke, J. Natl. Canc. Inst. 53: 333-1336 (1974).

35 While T-cell mediated immune responses were observed for the types of tumor described supra, spontaneous tumors were thought to be generally non-immunogenic. These were therefore believed not to present antigens which provoked a response to the tumor in the tumor carrying subject. See Hewitt, et al., Brit. J. Cancer 33: 241-259 (1976).

40 The family of tumor antigen presenting cell lines are immunogenic variants obtained by mutagenesis of mouse tumor cells or cell lines, as described by Boon et al., J. Exp. Med.

5 152: 1184-1193 (1980), the disclosure of which is incorporated
by reference. To elaborate, tum⁻ antigens are obtained by
mutating tumor cells which do not generate an immune response
in syngeneic mice and will form tumors (i.e., "tum⁺" cells).
10 When these tum⁺ cells are mutagenized, they are rejected by
syngeneic mice, and fail to form tumors (thus "tum⁻"). See
Boon et al., Proc. Natl. Acad. Sci. USA 74: 272 (1977), the
disclosure of which is incorporated by reference. Many tumor
types have been shown to exhibit this phenomenon. See, e.g.,
Frost et al., Cancer Res. 43: 125 (1983).

15 It appears that tum⁻ variants fail to form progressive
tumors because they elicit an immune rejection process. The
evidence in favor of this hypothesis includes the ability of
"tum⁻" variants of tumors, i.e., those which do not normally
form tumors, to do so in mice with immune systems suppressed
20 by sublethal irradiation, Van Pel et al., Proc. Natl. Acad.
Sci. USA 76: 5282-5285 (1979); and the observation that
intraperitoneally injected tum⁻ cells of mastocytoma P815
multiply exponentially for 12-15 days, and then are eliminated
in only a few days in the midst of an influx of lymphocytes
25 and macrophages (Uyttenhove et al., J. Exp. Med. 152: 1175-
1183 (1980)). Further evidence includes the observation that
mice acquire an immune memory which permits them to resist
subsequent challenge to the same tum⁻ variant, even when
immunosuppressive amounts of radiation are administered with
30 the following challenge of cells (Boon et al., Proc. Natl.
Acad. Sci. USA 74: 272-275 (1977); Van Pel et al., supra;
Uyttenhove et al., supra). Later research found that when
spontaneous tumors were subjected to mutagenesis, immunogenic
variants were produced which did generate a response. Indeed,
35 these variants were able to elicit an immune protective
response against the original tumor. See Van Pel et al., J.
Exp. Med. 157: 1992-2001 (1983). Thus, it has been shown that
it is possible to elicit presentation of a so-called "tumor
rejection antigen" in a tumor which is a target for a
40 syngeneic rejection response. Similar results have been
obtained when foreign genes have been transfected into

5 spontaneous tumors. See Fearson et al., Cancer Res. 48: 2975-1980 (1988) in this regard.

A class of antigens has been recognized which are presented on the surface of tumor cells and are recognized by cytotoxic T cells, leading to lysis. This class of antigens will be referred to as "tumor rejection antigens" or "TRAs" hereafter. TRAs may or may not elicit antibody responses. The extent to which these antigens have been studied, has been via cytolytic T cell characterization studies in vitro i.e., the study of the identification of the antigen by a particular cytolytic T cell ("CTL" hereafter) subset. The subset proliferates upon recognition of the presented tumor rejection antigen, and the cells presenting the antigen are lysed. Characterization studies have identified CTL clones which specifically lyse cells expressing the antigens. Examples of this work may be found in Levy et al., Adv. Cancer Res. 24: 1-59 (1977); Boon et al., J. Exp. Med. 152: 1184-1193 (1980); Brunner et al., J. Immunol. 124: 1627-1634 (1980); Maryanski et al., Eur. J. Immunol. 124: 1627-1634 (1980); Maryanski et al., Eur. J. Immunol. 12: 406-412 (1982); Palladino et al., Canc. Res. 47: 5074-5079 (1987). This type of analysis is required for other types of antigens recognized by CTLs, including major histocompatibility antigens, the male specific H-Y antigens, and a class of antigens, referred to as "tum-" antigens, and discussed herein.

A tumor exemplary of the subject matter described supra is known as P815. See DePlaen et al., Proc. Natl. Acad. Sci. USA 85: 2274-2278 (1988); Szikora et al., EMBO J 9: 1041-1050 (1990), and Sibille et al., J. Exp. Med. 172: 35-45 (1990), the disclosures of which are incorporated by reference. The P815 tumor is a mastocytoma, induced in a DBA/2 mouse with methylcholanthrene and cultured as both an in vitro tumor and a cell line. The P815 line has generated many tum⁻ variants following mutagenesis, including variants referred to as P91A (DePlaen, supra), 35B (Szikora, supra), and P198 (Sibille, supra). In contrast to tumor rejection antigens - and this is a key distinction - the tum⁻ antigens are only present after

5 the tumor cells are mutagenized. Tumor rejection antigens are present on cells of a given tumor without mutagenesis. Hence, with reference to the literature, a cell line can be tum⁺, such as the line referred to as "P1", and can be provoked to produce tum⁻variants. Since the tum⁻ phenotype differs from that of the parent cell line, one expects a difference in the DNA of tum⁻ cell lines as compared to their tum⁺ parental lines, and this difference can be exploited to locate the gene of interest in tum⁻ cells. As a result, it was found that genes of tum⁻ variants such as P91A, 35B and P198 differ from their normal alleles by point mutations in the coding regions of the gene. See Szikora and Sibille, supra, and Lurquin et al., Cell 58: 293-303 (1989). This has proved not to be the case with the TRAs of this invention. These papers also demonstrated that peptides derived from the tum⁻ antigen are presented by the L^d molecule for recognition by CTLs. P91A is presented by L^d, P35 by D^d and P198 by K^d.

Prior patent applications PCT/US92/04354, U.S. Serial No. 807,043; 764,364; 728,838 and 705,702, all of which are incorporated by reference and U.S. Patent No. 5,342,774, describe inventions involving, inter alia, genes and other nucleic acid molecules which code for various TRAPs, which are in turn processed to tumor rejection antigen, or "TRAs". SEQ ID NOS: 1-26 which are a part of the subject application present sequences of genes coding for various TRAPs, and the TRA referred to hereafter as MZ2E, which is derived from MAGE-1 TRAP (SEQ ID NO: 26).

The genes are useful as a source for the isolated and purified tumor rejection antigen precursor and the TRA themselves, either of which can be used as an agent for treating the cancer for which the antigen is a "marker", as well as in various diagnostic and surveillance approaches to oncology, discussed infra. It is known, for example, that tum⁻ cells can be used to generate CTLs which lyse cells presenting different tum⁻ antigens as well as tum⁺ cells. See, e.g., Maryanski et al., Eur. J. Immunol 12: 401 (1982); and Van den Eynde et al., Modern Trends in Leukemia IX (June

5 1990), the disclosures of which are incorporated by reference. The tumor rejection antigen precursor may be expressed in cells transfected by the gene, and then used to generate an immune response against a tumor of interest.

10 In the parallel case of human neoplasms, it has been observed that autologous mixed lymphocyte-tumor cell cultures ("MLTC" hereafter) frequently generate responder lymphocytes which lyse autologous tumor cells and do not lyse natural killer targets, autologous EBV-transformed B cells, or autologous fibroblasts (see Anichini et al., Immunol. Today 8: 15 385-389 (1987)). This response has been particularly well studied for melanomas, and MLTC have been carried out either with peripheral blood cells or with tumor infiltrating lymphocytes. Examples of the literature in this area including Knuth et al., Proc. Natl. Acad. Sci. USA 86: 2804- 20 2802 (1984); Mukherji et al., J. Exp. Med. 158: 240 (1983); Hérin et al., Int. J. Canc. 39: 390-396 (1987); Topalian et al., J. Clin. Oncol 6: 839-853 (1988). Stable cytolytic T cell clones have been derived from MLTC responder cells, and these clones are specific for the tumor cells. See Mukherji et al., 25 supra, Hérin et al., supra, Knuth et al., supra. The antigens recognized on tumor cells by these autologous CTLs do not appear to represent a cultural artifact, since they are found on tumor cells in vivo. Topalian et al., supra; Degiovanni et al., Eur. J. Immunol. 20: 1865-1868 (1990). These 30 observations, coupled with the techniques used herein to isolate the genes for specific murine tumor rejection antigen precursors, have led to the isolation of nucleic acid sequences coding for tumor rejection antigen precursors of TRAs presented on human tumors. It is now possible to isolate 35 the nucleic acid sequences which code for tumor rejection antigen precursors, including, but not being limited to those most characteristic of a particular tumor, with ramifications that are described infra.

40 Additional work has focused upon the presentation of TRAs by the class of molecules known as major histocompatibility complexes, or "MHCs". Human forms of these molecules are

5 "human leukocyte antigens" or "HLAs". This work has resulted
in several unexpected discoveries regarding the field.
Specifically in U.S. patent application Serial Number 938,334,
now U.S. Patent No. _____ the disclosure of which is
10 incorporated by reference, nonapeptides are taught which are
presented by the HLA-A1 molecule. The reference teaches that
given the known specificity of particular peptides for
particular HLA molecules, one should expect particular
peptides to bind one HLA molecule. These peptides, presented
15 herein as SEQ ID NOS: 27-34 are also presented in Traversari
et al., J. Exp. Med. 176: 1453-1457 (1992). This is
important, because different individuals possess different HLA
phenotypes. As a result, while identification of particular
peptides or of particular motifs, and the peptides which are
members thereof, as being partners for a specific HLA molecule
20 has diagnostic and therapeutic ramifications, these are only
relevant for individuals with that particular HLA phenotype.
There is a need for further work in the area, because cellular
abnormalities are not restricted to one particular HLA
phenotype, and targeted therapy requires some knowledge of the
25 phenotype of the abnormal cells at issue.

In U.S. Patent Application Serial Number 008,446, filed
January 22, 1993 and incorporated by reference, the fact that
the MAGE-1 expression product is processed to a second TRA is
disclosed. This second TRA is presented by HLA-Cw* 1601
30 molecules. The disclosure shows that a given TRAP can yield
a plurality of TRAs.

In U.S. Patent Application Serial Number 994,928, filed
December 22, 1992, and incorporated by reference herein,
tyrosinase is described as a tumor rejection antigen
precursor. This is a well known molecule as per Kwon, U.S.
35 Patent No. 4,898,814. This reference discloses that a
molecule which is produced by some normal cells (e.g.,
melanocytes), is processed in tumor cells to yield a tumor
rejection antigen that is presented by HLA-A2 molecules. The
peptide presented thereby is described in U.S. Application
40 Serial No. 54,714, filed April 28, 1993. SEQ ID NO: 35 sets

5 forth this peptide. Additional tyrosinase derived peptides presented by HLA molecules are set forth in Serial Nos. 203,054, and 233,305 filed February 28, 1994 and April 26, 1994 and incorporated by reference (SEQ ID NOS: 36-41).

10 Other peptides which are TRAs are described in additional patent applications. U.S. Patent Application Serial No. 195,186, filed February 14, 1994, and incorporated by reference herein, sets forth three peptides (SEQ ID NOS: 42-44 herein), which are derived from MAGE-1 and which complex with HLA-Cw* 1601. Serial No. 196,630, filed February 15, 1994, 15 discloses an unrelated tumor rejection antigen precursor, the so-called "BAGE" gene, and peptides derived therefrom, which are processed and then presented by HLA-Cw* 1601. These are set forth as SEQ ID NOS: 45-48, and this application is incorporated by reference. SEQ ID NO: 48 is the tumor 20 rejection antigen. Additional coding sequences for a tumor rejection antigen precursor are set forth in Serial No. 32,978, filed March 18, 1993 and incorporated by reference. These are included herein as SEQ ID NOS: 49 and 50. A more extended sequence for this gene is set forth in Serial No. 25 272,351, filed July 8, 1994 incorporated by reference, and is SEQ ID NO: 51. In Serial No. 96,039, filed July 22, 1993, the sequence of tumor rejection antigen precursor GAGE is set forth. See SEQ ID NO: 52 for this information.

30 A series of peptides which provoke lysis by cytolytic T cells when presented by MHC molecules are set forth in Serial No. 217,186, Serial No. 08/217,188, and Serial No. 217,187, all filed on March 24, 1994, and all of which are incorporated by reference herein. The first of these applications discloses MAGE-3 derived peptides presented by HLA-A2. Five 35 peptides are of interest. These are repeated here as SEQ ID NOS: 53-57. The second application presents 11 sequences derived from MAGE-2, believed to complex with HLA-A2.1 molecules (SEQ ID NOS: 58-68). The last of these applications discloses two additional peptides (SEQ ID NOS: 69 and 70) 40 derived from MAGE-3 which complex to HLA-A2. Serial No. 190,411, filed April 1, 1994 and incorporated by reference,

5 sets forth three peptides (SEQ ID NO: 71-73), derived from
MAGE-1, which are immunogenic in that they provoke production
of antibodies in a host animal to which they have been
administered. Seial No. 253,503, filed June 3, 1994 and
10 incorporated by reference, teaches a further tumor rejection
antigen precursor gene (SEQ ID NO:74), and a peptide, derived
therefrom (SEQ ID NO:75), whch is presented by HLA-B44
molecules. Further in the application of Coulie, Ikeda and
Boon-Falleur, filed concurrently, a sequence coding for a
15 tumor rejection antigen precursor known as DAGE (SEQ ID NO:76)
is set forth. DAGE is found almost universally on tumor
cells, and only on testis cells with respect to normal cell
expression. This makes it especially useful for cancer
diagnosis and in the applications disclosed herein. The above
20 listing should not be presumed to be exhaustive of the TRAP
and TRA literature, but is presented to show its diversity and
the fact that these materials not only provoke T cell
proliferation, but also stimulate production of antibodies.
It is well known that antibody producing cells can be used as
a source to produce hybridomas, which in turn produce
25 monoclonal antibodies. Thus, when the term "antibodies" is
used herein, it encompasses both polyclonal and monoclonal
antibodies.

The parent applications to the present case, including
Serial No. 142,368 and Serial No. 190,411, both discuss the
30 usefulness of combining TRAPs or TRAs with various materials
as adjuvants, to produce vaccines, immunogenic compositions,
etc. Adjuvants, broadly defined, are substances which promote
immune responses. Frequently, the adjuvant of choice is
Freund's complete adjuvant, or killed B. pertussis organisms,
35 used in combination with alum precipitated antigen. A general
discussion of adjuvants is provided in Goding, Monoclonal
Antibodies: Principles & Practice (Second edition, 1986), at
pages 61-63, which are incorporated by reference herein.
Goding notes, however, that when the antigen of interest is of
40 low molecular weight, or is poorly immunogenic, coupling to an
immunogenic carrier is recommended. Such molecules, according

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5 to Goding, generally have molecular weights below about 1000. Among the carriers suggested by Goding, at page 283, are keyhole limpet hemocyanin, bovine serum albumin, ovalbumin, and fowl immunoglobulin.

10 What is problematic about such carriers, however, is that frequently they are also immunogenic themselves. Thus, the immune response may be a general one, with part, most, or all of it being directed against the carrier molecule rather than the immunogen itself.

15 Exemplary of developments in the art as they relate to adjuvants is U.S. Patent No. 5,057,540 to Kensil, et al, the disclosure of which is incorporated by reference herein. Kensil et al disclose the preparation of various saponin extracts, which are useful as adjuvants in immunogenic compositions. As natural products, the extracts are not
20 completely defined. Kensil, et al do provide a complete and enabling disclosure for how various extracts, including QA-7, QA-19, and QA-21 (also referred to as QS-21) are prepared. Experiments are set forth in which bovine serum albumin ("BSA") was combined with various extracts (examples 8 and 9),
25 and where feline leukemia virus recombinant glycoprotein "gp70RΔ" was tested, following absorption to aluminum hydroxide (alum). The two immunogens tested, however, are expected to be immunogenic in their own right (gp70RΔ has a molecular weight of 70 kd, and serum albumin has about the same
30 molecular weight). No experiments were carried out at all on molecules which should, per se, be considered to be poorly or even non-immunogenic, and thus would be expected to require the use of alum absorption or the use of haptenic carriers for provocation of a response.

35 In PCT Application WO9219758, which corresponds to defensive publication 7697275, which is incorporated by reference herein, an adjuvant referred to as "MTP-MF59" is disclosed. This adjuvant is used in connection with a Plasmodium falciparum protein, "Pfs-25-B". This combination
40 is described as a transmission blocking vaccine. The P. falciparum protein is itself large enough to be immunogenic.

5 Thus, none of the art shows that the improved adjuvants can be used in combination with presumptively non-immunogenic proteins and peptides to yield immunologically effective compositions. This is especially true for TRAP and TRA molecules, as outlined supra.

10 It has now been found, surprisingly, that compositions comprising tumor rejection antigen precursors or tumor rejection antigens can be made which, when administered to a subject animal, provoke an immunogenic response. In especially preferred embodiments the immunogenic portion of
15 the composition consists of TRAP or, more preferably TRA molecules, of one or more types, and an adjuvant. Especially preferred are compositions where the adjuvant is QS21, as is disclosed in the Kensil, et al patent, incorporated by reference supra.

20 The immunogens of this invention consist of TRAPs or TRAs, meaning that they do not include haptens, carriers, precipitated alum, or any of the materials normally associated with materials which are or are expected to be poorly
25 immunogenic. In especially preferred embodiments, the compositions consist essentially of the immunogen and the adjuvant.

The invention is described in greater detail in the disclosure which follows.

DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

Example

30 The following example demonstrates the use of peptide MZ2E (SEQ ID NO: 26) in connection with adjuvant QS-21. It is to be understood, however, that one may routinely substitute proteins or peptides (the first component of the composition)
35 and adjuvants (the second component of the composition). The unexpected effect of the combination of MZ2E and QS21 should occur in the alternate combinations, i.e., when other peptides are used.

40 Subjects tested are patients with stage IV melanoma or high risk stage III malignant melanoma. Stage IV patients have a median survival time of one year following diagnosis,

5 and only a 15% chance of long-term survival (Balch, et al, Cutaneous Melanoma, J.b. Lippincott, Philadelphia, 1992). The standard therapy for these patients includes treatment with decarbazine or drug combinations with decarbazine; however, response rates only range from 8-25%, and there is no evidence
10 of the treatment extending survival. Balch et al, supra. Patients with high risk Stage III melanoma (pT4 thick truncal primary tumors or extremity melanomas, with five or more positive regional lymph nodes) have a median survival of 1-2 years following onset, and a 19% chance of long term survival.
15 Balch, et al, supra.

Twelve patients are used in the study, all of whom have either Stage IV or high risk Stage III malignant melanoma in accordance with the criteria provided supra, confirmed by review of histology.

20 The patients fulfil the following additional criteria:

- (i) complete recovery from surgery;
- (ii) no chemotherapy or immunotherapy, within the four weeks preceding immunization;
- (iii) expected survival of at least three months;
- 25 (iv) Karnofsky Performance Status of 60 or more;
- (v) Laboratory results as follows:
 - granulocytes \geq 2,500/min³
 - lymphocytes \geq 700/min³
 - platelets \geq 100,000/min³
 - 30 serum creatinine \leq 2.0 mg/100 ml
 - serum bilirubin \leq 2.0 mg/100 ml
- (vi) for MZ2E immunization, patients are positive for HLA-A1;
- (vii) for MZ2E immunization, the patients' tumors express
35 MAGE-1;
- (viii) they be over 19 years old and be capable of giving informed consent in writing.

Any potential subjects who satisfy any of the following
40 criteria are excluded:

- (i) clinically significant heart disease;

- 5 (ii) other serious illness, such as active infection
 requiring antibiotics, or bleeding disorders;
- (iii) treatment with antihistamines, N-SAIDS, or corti-
 costeroids;
- 10 (iv) immunodeficiency, splenectomy, or radiation therapy
 to the spleen;
- (v) pregnancy or lactation;
- (vi) women of childbearing age who do not use effective
 methods of contraception.

15 All subjects are treated as outpatients. They are immunized,
subcutaneously, with MZ2E (30 ug or 300 ug) and QS21 (100 ug),
in 0.3 ml phosphate buffered saline, pH 7.4. Six patients
receive 30 ug of peptide, and six receive 300 ug. The first
20 injection is into the deltoid region of the anterior aspect of
the thigh, and the site of injection is changed with follow up
injections. No injections are given into limbs where draining
lymph nodes have been surgically removed or irradiated.

 Injections are given at day 1, and then at days 8, 15,
22, and 57. Patients are monitored over a course of 12 weeks,
25 unless intervention is required (as determined by the
investigator). Any patients who show stabilization or tumor
response remain in the study until disease progression is
evidenced. Patients may also be removed from the study or
receive different doses of the peptide, if toxicity reactions
30 are observed.

 The patients show response as follows. In a complete
response, all signs, symptoms, biochemical and imaging
evidence of tumor disappear for a period of at least 30 days.
In a partial response, there is a decrease in size of all
35 measurable tumors of at least 50% of the sum of products of
the greatest and perpendicular diameters for at least 30 days,
without the appearance of new lesions or progression of any
new lesions. In a minor response, there is a decrease in size
of all measurable tumors of at least 25% of the sum of
40 products of greatest and perpendicular diameters, for at least
30 days, without appearance of new lesions or progression of

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5 any lesion. In stable disease, there is a change of less than 25% of the sum of products of greatest and perpendicular diameters, for at least 30 days, without the appearance of new lesions or progression of lesions. In progression of the disease, there is appearance of new tumors, or an increase in
10 the size of measurable tumors of at least 50% of the sum of the product of greatest and perpendicular diameter.

The foregoing example demonstrates a composition comprising an amount of a tumor rejection antigen, i.e., MZ2E, and an adjuvant, i.e., QS21, and the use of the composition in
15 the in vivo treatment of cancer (i.e., melanoma). The tumor rejection antigen is used in an amount sufficient to provoke an immune response against tumor cells which present it on their surface.

The compositions of the invention comprise any tumor rejection antigen precursor ("TRAP") or tumor rejection antigen ("TRA"), in combination with a pharmaceutically acceptable adjuvant. Preferred embodiments of the invention utilize the TRAPs and TRAs discussed supra and set forth in
20 SEQ ID NO: 65, as well as the adjuvants described in the Background section.

As will be seen from the foregoing discussion, an important aspect of the invention is stimulation of proliferation of T cells. This can be an initial stimulation or an augmentation of a prior stimulation. In particular, it
30 is desirable to stimulate cytolytic T cells which present peptides, such as the TRAs described herein, on their surfaces. The cytolytic T cells recognize these complexes of MHC and peptide, bind thereto via their receptor, and proliferate. They also lyse the recognized cells. This
35 response can be used not only in vivo, but in vitro, as it is well established that cytolytic T cells specific for particular complexes of MHC and peptide are present in the blood of subjects who have experienced cell transformation. By contacting a blood sample of individuals in vitro with the
40 peptide of interest and cells which present the MHC molecule of interest, any cytolytic T cells in the blood sample will

5 expand, i.e., proliferate. This proliferation can be measured via any of the well known assays designed therefor. Especially preferred are the radioactive chromium (^{51}Cr) release assay, and the measurement of release of tumor necrosis factor (TNF).

10 The compositions are also useful as stimulators of B cell proliferation, or antibody production. Again, it is well known that B cells produce antibodies, and the size of their targets are well within the sizes of the tumor rejection antigens, and certainly the tumor rejection antigen precursors. As with T cells, the stimulation may be "ab initio", or an augmentation of a prior response, in vitro or in vivo.

20 The amount of TRAP or TRA used will vary, depending upon the purpose of the immunization and the subject to which it is administered. For example, in the case of generating murine antibodies which can then be used, e.g., to diagnose for the presence of cancer cells presenting a TRA, the amount of protein or peptide may be less than that used in a course of in vivo therapy, such as that described in the example, supra. In general, a preferred dose can range from about 1 ug to about 750 ug of protein or peptide per dose. In a preferred embodiment, the range is from about 10 ug to about 500 ug. Most preferably, anywhere from about 30 ug to about 300 ug per dose may be used. Of course, in the context of the therapeutic aspect of the invention, the investigator will modify the dose, as a six month old infant will require dosing different from a full grown man, e.g. The mode of administration may vary, with preferred forms being oral, subcutaneous, intramuscular, intravenous and intraperitoneal administration.

35 The choice of TRAP or TRA protein or peptide in the composition will depend upon parameters determinable by the artisan. It is art recognized, for example, that different TRAs are presented by the various MHC molecules. As such, if a subject is typed, using well known techniques, as presenting HLA-A2 molecules on the surface of tumor cells, one will use

5 a TRA presented by HLA-A2 molecules rather than one presented
by, e.g., HLA-Cw* 1601. Similarly, using techniques such as
polymerase chain reaction ("PCR"), lysis studies, and other
assay methodologies which are well known in the art, one can
determine which tumor rejection antigen precursor gene or
10 genes are being expressed by a subject patient. This will
lead to the decision as to what protein or peptide to use.
Again, by way of example, if a subject's tumor cells are
expressing MAGE-3 but not MAGE-1, the peptide used in
immunization should be derived from MAGE-3, and not MAGE-1.

15 While the molecules discussed herein are referred to as
"tumor" rejection antigens and "tumor" rejection antigen
precursors, it is intended that their use, in a therapeutic
and also a diagnostic context, extends beyond cancer per se.
The art is familiar with pathological conditions, such as
20 displastic nevis, which are not cancer per se, but where the
cells of the afflicted individuals are in fact characterized
by transformation. Any and all such conditions are within the
intended ambit of the invention.

Other aspects of the invention will be clear to the
25 skilled artisan and need not be reiterated here.

The terms and expressions which have been employed are
used as terms of description and not of limitation, and there
is no intention in the use of such terms and expressions of
excluding any equivalents of the features shown and described
30 or portions thereof, it being recognized that various
modifications are possible within the scope of the invention.

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Boon-Falleur, Thierry; van den Eynde, Benoit;
van der Bruggen, Pierre
- (ii) TITLE OF INVENTION: COMPOSITIONS CONTAINING TUMOR REJECTION
ANTIGEN PRECURSORS OR TUMOR REJECTION ANTIGENS, AND AN
ADJUVANT AND/OR GROWTH FACTOR
- (iii) NUMBER OF SEQUENCES: 76
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Felfe & Lynch
- (B) STREET: 805 Third Avenue
- (C) CITY: New York City
- (D) STATE: New York
- (E) COUNTRY: USA
- (F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
- (B) COMPUTER: IBM PS/2
- (C) OPERATING SYSTEM: PC-DOS
- (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/315,961
- (B) FILING DATE: 30-SEPTEMBER-1994
- (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: PCT/US92/04354
- (B) FILING DATE: 22-MAY-1992
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/938,334
- (B) FILING DATE: 31-AUGUST-1992
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/008,446
- (B) FILING DATE: 22-JANUARY-1993
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/054,714
- (B) FILING DATE: 28-APRIL-1993

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- 5 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/203,054
(B) FILING DATE: 28-FEBRUARY-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/233,305
10 (B) FILING DATE: 26-APRIL-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/195,186
(B) FILING DATE: 14-FEBRUARY-1994
- (vii) PRIOR APPLICATION DATA:
15 (A) APPLICATION NUMBER: 08/196,630
(B) FILING DATE: 15-FEBRUARY-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/032,978
(B) FILING DATE: 18-MARCH-1993
- 20 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/217,186
(B) FILING DATE: 24-MARCH-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/217,187
25 (B) FILING DATE: 24-MARCH-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/217,188
(B) FILING DATE: 24-MARCH-1994
- (vii) PRIOR APPLICATION DATA:
30 (A) APPLICATION NUMBER: 08/190,411
(B) FILING DATE: 1-APRIL-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/253,503
(B) FILING DATE: 3-JUNE-1994
- 35 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Hanson, Norman D.
(B) REGISTRATION NUMBER: 30,946
(C) REFERENCE/DOCKET NUMBER: LUD 5370
- (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: (212) 688-9200
(B) TELEFAX: (212) 838-3884

19

5 (2) INFORMATION FOR SEQUENCE ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

15 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60
 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT 120
 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG 180
 CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240
 CCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG CATGCATTGT 360
 20 GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420
 TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC 462

25 (2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

35 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT 48
 Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
 5 10 15
 GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA 96
 Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
 20 25 30
 40 GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA 144
 Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr

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5	35	40	45	
	AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG	192		
	Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln			
	50	55	60	
10	TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC	240		
	Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser			
	65	70	75	80
	TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC	288		
	Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr			
	85	90	95	
15	GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	336		
	Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp			
	100	105	110	
	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG	384		
	Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu			
20	115	120	125	
	GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG	432		
	Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met			
	130	135	140	
	GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG	480		
25	Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys			
	145	150	155	160
	AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC	528		
	Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe			
	165	170	175	
30	CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT	576		
	Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys			
	180	185	190	
	GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG	624		
	Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu			
35	195	200	210	
	GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	672		
	Glu Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro			
	220	225	230	235
40	TAG			675

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(2) INFORMATION FOR SEQUENCE ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT    60
TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT    120
TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAAC TTT CATATGATAC    180
ATAGGATTAC ACTTGACCT GTTAAAAATA AAAGTTTGAC TTGCATAC                    228
```

(2) INFORMATION FOR SEQUENCE ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1365 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT    50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT    100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG    150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT    200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA    250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT    300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG    350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG    400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT    450
ACCCTTTGTG CC                                                462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA    504
```

22

5	GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
	TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
	TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
	ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
	TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
10	GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC	756
	GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
	GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
	GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT	924
15	GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT	966
	TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG	1008
	AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT	1050
	GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG	1092
	GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	1134
20	TAG	1137
	GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG	1187
	TTGTTTTTTT TTCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA	1237
	ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT	1287
	CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTAACCT	1337
25	GTAAAAATA AAAGTTTGAC TTGCATAC	1365

(2) INFORMATION FOR SEQUENCE ID NO: 5:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4698 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

	ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
	GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT	100
40	CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG	150
	AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCCTT	200

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5	CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA	250
	CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
	AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG	350
	CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG	400
	CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
10	ACCCTTTGTG CC	462
	ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
	GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
	TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
	TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
15	ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
	TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
	GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC	756
	GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
20	GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
	GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T	916
	GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA	966
	CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC	1016
	TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC	1066
25	CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCACCTTG CCTCTGGAGC	1116
	TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC	1166
	TCCCCCTCGG CTCAACTTTT CGTGCCCTTCT GCTCTCTGAT CCCCACCCTC	1216
	TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCCTCCCC TTCCTGTTCC	1266
	CCTTTTTCGG CTTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT	1316
30	TCACCAGCTT TGCTCTCCCT GCTCCCCCTC CCCTTTTGCA CTTTTTCTTT	1366
	TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT	1416
	CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG	1466
	TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT	1516
	CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT	1566
35	TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC	1616
	TCACTCTGTA GACCAGGCTG GCCTCAAAC T CAGAAATCTG CCTGCCTCTG	1666
	CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG	1716
	GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT	1766
	AACTCCCTTT TTGGCACCTT TCCTTTACAG GACCCCTCC CCCTCCCTGT	1816
40	TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCCCTC TCCTGCTCC	1866
	CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTGCTTTCT	1916

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5	GCCCCGTTCC CCTTTTTTGT GCCTTTCCTC CTGGCTCCCC TCCACCTTCC	1966
	AGCTCACCTT TTTGTTTGT TGGTTGTTG GTTGTGTTGTT TGCTTTTTT	2016
	TTTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCCCCC TCCGGCTTCC	2066
	CCTCTGTGTG CCTTTCCTGT TCCCTCCCCC TCGCTGGCTC CCCCTCCCTT	2116
	TCTGCCTTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTTT	2166
10	CTTTTCTAGA CTCCCCCTC CAGGCTTGCT GTTTGCTTCT GTGCACTTTT	2216
	CCTGACCCTG CTCCCCCTCC CCTCCCAGCT CCCCCCTCTT TTCCCACCTC	2266
	CCTTTCTCCA GCCTGTCACC CCTCCTTCTC TCCTCTCTGT TTCTCCCACT	2316
	TCCTGCTTCC TTTACCCCTT CCCTCTCCCT ACTCTCCTCC CTGCCTGCTG	2366
	GACTTCCTCT CCAGCCGCCC AGTTCCTGC AGTCCTGGAG TCTTTCCTGC	2416
15	CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCTTTC ACTCTCCCTT	2466
	ATGTGTCTCT CTTCTATCT ATCCCTTCTT TTCTGTCCCC TCTCCTCTGT	2516
	CCATCACCTC TCTCCTCCCT TCCCTTTCCT CTCTCTTCCA TTTTCTTCCA	2566
	CCTGCTTCTT TACCCTGCCT CTCCCATTGC CCTCTTACCT TTATGCCCAT	2616
	TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTCCCT CACATCTTCC	2666
20	ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC	2716
	TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TCCCCTATG CCCTCTACTC	2766
	TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGCC	2816
	CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC	2866
	ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCAA ATCAGCAGGA	2916
25	AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGCC	2966
	AAGTGGCTCC TATAACCCTA AGTACCAAGG GAGAAAGTGA TGGTGAAGTT	3016
	CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAATG	3066
	CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA	3116
	GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCACG	3166
30	TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTGAGA	3216
	TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTTA	3266
	GGCTAAAGAT ACTTGGAACC ATAGAAGCGT TGTTAAATA CTGCTTTCTT	3316
	TTGCTAAAAT ATTCTTTCTC ACATATTCAT ATTCTCCAG	3355
	GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT	3396
35	AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT	3438
	ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA	3480
	AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA	3522
	GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC	3564
	TTC TCA CCT TAG	3576
40	GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGTA	3626
	GCTAAGAGCA TCTTTTAAA AAATATTATT GGTAAGCTAA ACAATTGTTA	3676

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5	TCTTTTACATA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA	3726
	CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT	3776
	GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA	3826
	GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG	3876
	TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT	3926
10	TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCTG	3976
	TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT	4026
	CTTAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTCCT	4076
	TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTGA GATTTCTTAA	4126
	AATGTTTTTT AAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA	4176
15	GTAAGTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA	4226
	GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC	4276
	CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC	4326
	ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT	4376
	ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA	4426
20	AGTCAGGAGT GTATTCTAAT AAGTGTGCT TATCTCTTAT TTTCTTCTAC	4476
	AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT	4526
	TTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA GAAAATTTGA	4576
	TTTGTTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT	4626
	GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTATAA	4676
25	AATAAAAGTT TGACTTGCAT AC	4698

(2) INFORMATION FOR SEQUENCE ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|---------------------------|
| 30 | (A) LENGTH: 9 amino acids |
| | (B) TYPE: amino acid |
| | (C) STRANDEDNESS: single |
| | (D) TOPOLOGY: linear |

(ii) MOLECULE TYPE: protein

- | | |
|----|--|
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6: |
|----|--|

Leu Pro Tyr Leu Gly Trp Leu Val Phe

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- 5 (2) INFORMATION FOR SEQUENCE ID NO: 7:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2419 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
10 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

15	GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG	50
	GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC	100
	TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG	150
	GGCCCGTGGA TTCCTCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT	200
	TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT	250
20	GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA	300
	CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT	350
	CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC	400
	TTCCTCCTTC AGGTTTTTTCAG GGGACAGGCC AACCCAGAGG ACAGGATTCC	450
	CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG	500
25	TTAGAGTCTC CAAGGTTTCAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT	550
	CTCTCCCCAG GCCTGTGGGT CTTCAATTGCC CAGCTCCTGC CCACACTCCT	600
	GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC	650
	ACTGCAAGCC TGAGGAAGCC CTTGAGGCCC AACAAGAGGC CCTGGGCCTG	700
	GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGGCAC	750
30	CCTGGAGGAG GTGCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC	800
	AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA	850
	CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG	900
	TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT	950
	TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG	1000
35	GCAGAAATGC TGGAGAGTGT CATCAAAAAT TACAAGCACT GTTTTCCTGA	1050
	GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG	1100
	TGAAGGAAGC AGACCCACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA	1150
	GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC	1200
	AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GGCGGCCATG	1250
40	CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT	1300
	GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA	1350

5	TTTGGTGCAG GAAAAGTACC TGGAGTACGG CAGGTGCCGG ACAGTGATCC	1400
	CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT	1450
	ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGCAAG AGTTCGCTTT	1500
	TTCTTCCCAT CCCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT	1550
	CTGAGCATGA GTTGCAGCCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC	1600
10	ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCTCGTG TGACATGAGG	1650
	CCCATTCTTC ACTCTGAAGA GAGCGGTCAG TGTTCCTCAGT AGTAGGTTTC	1700
	TGTTCTATTG GGTGACTTGG AGATTTATCT TTGTTCTCTT TTGGAATTGT	1750
	TCAAATGTTT TTTTAAAGG GATGGTTGAA TGAAGTTCAG CATCCAAGTT	1800
	TATGAATGAC AGCAGTCACA CAGTTCTGTG TATATAGTTT AAGGGTAAGA	1850
15	GTCTTGTT TTATTCAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG	1900
	ATAATAACAG CAGTGGAATA AGTACTTAGA AATGTGAAAA ATGAGCAGTA	1950
	AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATTCTTGC	2000
	CTTATACCTC AGTCTATTCT GTAAAATTTT TAAAGATATA TGCATACCTG	2050
	GATTCCTTG GCTTCTTTGA GAATGTAAGA GAAATTAAT CTGAATAAAG	2100
20	AATCTTCCT GTTCACTGGC TCTTTTCTTC TCCATGCACT GAGCATCTGC	2150
	TTTTTGGAAG GCCCTGGGT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT	2200
	CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG	2250
	AGGTGGCAAG ATGTCCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA	2300
	GGGTGTGGGG CTCCGGGTGA GAGTGGTGGA GTGTCAATGC CCTGAGCTGG	2350
25	GGCATTTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT	2400
	AATGATCTTG GGTGGATCC	2419

- 30 (2) INFORMATION FOR SEQUENCE ID NO: 8:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 35 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (ix) FEATURE:
- (A) NAME/KEY: MAGE-1 gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

40

5	CCCGGGGCAC CACTGGCATC CCTCCCCCTA CCACCCCCAA TCCCTCCCTT	50
	TACGCCACCC ATCCAAACAT CTTACGCTC ACCCCCAGCC CAAGCCAGGC	100
	AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCCAG	150
	ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT	200
	CGGTCTGAGG GCGGCTTGA GATCGGTGGA GGAAGCGGG CCCAGCTCTG	250
10	TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC	300
	AGATAGAGGA CCCCAAATAA TCCCTTCATG CCAGTCCTGG ACCATCTGGT	350
	GGTGGACTTC TCAGGCTGGG CCACCCCCAG CCCCCTTGCT GCTTAAACCA	400
	CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG	450
	AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG	500
15	AGGGCTGAGG GTCCCTAAGA CCCCCTCCC GTGACCCAAC CCCCCTCCA	550
	ATGCTCACTC CCGTGACCCA ACCCCCTCTT CATTGTCATT CCAACCCCCA	600
	CCCCACATCC CCCACCCCAT CCCTCAACCC TGATGCCCAT CCGCCCAGCC	650
	ATTCCACCCCT CACCCCCACC CCCACCCCCA CGCCCCTCC CACCCCCACC	700
	CAGGCAGGAT CCGGTTCCCG CCAGGAAACA TCCGGGTGCC CGGATGTGAC	750
20	GCCACTGACT TGCGCATTGT GGGGCAGAGA GAAGCGAGGT TTCCATTCTG	800
	AGGGACGGCG TAGAGTTCGG CCGAAGGAAC CTGACCCAGG CTCTGTGAGG	850
	AGGCAAGGTG AGAGGCTGAG GGAGGACTGA GGACCCCGCC ACTCCAAATA	900
	GAGAGCCCCA AATATTCCAG CCCCGCCCTT GCTGCCAGCC CTGGCCCACC	950
	CGCGGGAAGA CGTCTCAGCC TGGGCTGCCC CCAGACCCCT GCTCCAAAAG	1000
25	CCTTGAGAGA CACCAGGTTT TTCTCCCCAA GCTCTGGAAT CAGAGGTTGC	1050
	TGTGACCAGG GCAGGACTGG TTAGGAGAGG GCAGGGCACA GGCTCTGCCA	1100
	GGCATCAAGA TCAGCACCCA AGAGGGAGGG CTGTGGGCCC CCAAGACTGC	1150
	ACTCCAATCC CCACTCCCAC CCCATTGCGA TTCCCATTCC CCACCCAACC	1200
	CCCATCTCCT CAGCTACACC TCCACCCCCA TCCCTACTCC TACTCCGTCA	1250
30	CCTGACCACC ACCCTCCAGC CCCAGCACCA GCCCCAACCC TTCTGCCACC	1300
	TCACCCTCAC TGCCCCAAC CCCACCCTCA TCTCTCTCAT GTGCCCCACT	1350
	CCCATCGCCT CCCCCATTCT GGCAGAATCC GGTGTTGCCCC TGCTCTCAAC	1400
	CCAGGGAAGC CCTGGTAGGC CCGATGTGAA ACCACTGACT TGAACCTCAC	1450
	AGATCTGAGA GAAGCCAGGT TCATTTAATG GTTCTGAGGG GCGGCTTGAG	1500
35	ATCCACTGAG GGGAGTGGTT TTAGGCTCTG TGAGGAGGCA AGGTGAGATG	1550
	CTGAGGGAGG ACTGAGGAGG CACACACCCC AGGTAGATGG CCCCAAAATG	1600
	ATCCAGTACC ACCCCTGCTG CCAGCCCTGG ACCACCCGGC CAGGACAGAT	1650
	GTCTCAGCTG GACCACCCCC CGTCCCGTCC CACTGCCACT TAACCCACAG	1700
	GGCAATCTGT AGTCATAGCT TATGTGACCG GGGCAGGGTT GGTCAGGAGA	1750
40	GGCAGGGCCC AGGCATCAAG GTCCAGCATC CGCCCGGCAT TAGGGTCAGG	1800
	ACCCTGGGAG GGAAGTGAAG GTTCCCCACC CACACCTGTC TCCTCATCTC	1850

SUBSTITUTE SHEET (RULE 26)

5	CACCGCCACC CCACTCACAT TCCCATACCT ACCCCCTACC CCCAACCTCA	1900
	TCTTGTGAGA ATCCCTGCTG TCAACCCACG GAAGCCACGG GAATGGCGGC	1950
	CAGGCACTCG GATCTTGACG TCCCCATCCA GGGTCTGATG GAGGGAAGGG	2000
	GCTTGAACAG GGCCTCAGGG GAGCAGAGGG AGGGCCCTAC TGCAGATGA	2050
	GGGAGGCCCTC AGAGGACCCA GCACCCTAGG ACACCGCACC CCTGTCTGAG	2100
0	ACTGAGGCTG CCACTTCTGG CCTCAAGAAT CAGAACGATG GGGACTCAGA	2150
	TTGCATGGGG GTGGGACCCA GGCCTGCAAG GCTTACGCGG AGGAAGAGGA	2200
	GGGAGGACTC AGGGGACCTT GGAATCCAGA TCAGTGTGGA CCTCGGCCCT	2250
	GAGAGGTCCA GGGCAGGGTG GCCACATATG GCCCATATTT CCTGCATCTT	2300
	TGAGGTGACA GGACAGAGCT GTGGTCTGAG AAGTGGGGCC TCAGGTCAAC	2350
15	AGAGGGAGGA GTTCCAGGAT CCATATGGCC CAAGATGTGC CCCCTTCATG	2400
	AGGACTGGGG ATATCCCCGG CTCAGAAAGA AGGGACTCCA CACAGTCTGG	2450
	CTGTCCCCTT TTAGTAGCTC TAGGGGGACC AGATCAGGGA TGGCGGTATG	2500
	TTCCATTCTC ACTTGTACCA CAGGCAGGAA GTTGGGGGGC CCTCAGGGAG	2550
	ATGGGGTCTT GGGGTAAAGG GGGGATGTCT ACTCATGTCA GGGGAATTGGG	2600
20	GGTTGAGGAA GCACAGGCGC TGGCAGGAAT AAAGATGAGT GAGACAGACA	2650
	AGGCTATTGG AATCCACACC CCAGAACCAA AGGGGTCAGC CCTGGACACC	2700
	TCACCCAGGA TGTGGCTTCT TTTTCACTCC TGTTTCCAGA TCTGGGGCAG	2750
	GTGAGGACCT CATTCTCAGA GGGTGA CTCA GGTCAACGTA GGGACCCCCA	2800
	TCTGGTCTAA AGACAGAGCG GTCCCAGGAT CTGCCATGCG TTCGGGTGAG	2850
25	GAACATGAGG GAGGACTGAG GGTACCCCAG GACCAGAACA CTGAGGGAGA	2900
	CTGCACAGAA ATCAGCCCTG CCCCTGCTGT CACCCCAGAG AGCATGGGCT	2950
	GGGCCGTCTG CCGAGGTCCT TCCGTTATCC TGGGATCATT GATGTCAGGG	3000
	ACGGGGAGGC CTTGGTCTGA GAAGGCTGCG CTCAGGTCAG TAGAGGGAGC	3050
	GTCCCAGGCC CTGCCAGGAG TCAAGGTGAG GACCAAGCGG GCACCTCACC	3100
30	CAGGACACAT TAATTCCAAT GAATTTTGAT ATCTCTTGCT GCCCTTCCCC	3150
	AAGGACCTAG GCACGTGTGG CCAGATGTTT GTCCCCTCCT GTCCTTCCAT	3200
	TCCTTATCAT GGATGTGAAC TCTTGATTG GATTTCTCAG ACCAGCAAAA	3250
	GGGCAGGATC CAGGCCCTGC CAGGAAAAAT ATAAGGGCCC TGC GTGAGAA	3300
	CAGAGGGGGT CATCCACTGC ATGAGAGTGG GGATGTCACA GAGTCCAGCC	3350
35	CACCCCTCCTG GTAGCACTGA GAAGCCAGGG CTGTGCTTGC GGTCTGCACC	3400
	CTGAGGGCCC GTGGATTCTT CTTCTGAG CTCCAGGAAC CAGGCAGTGA	3450
	GGCCTTGGTC TGAGACAGTA TCCTCAGGTC ACAGAGCAGA GGATGCACAG	3500
	GGTGTGCCAG CAGTGAATGT TTGCCCTGAA TGCACACCAA GGGCCCCACC	3550
	TGCCACAGGA CACATAGGAC TCCACAGAGT CTGGCCTCAC CTCCCTACTG	3600
40	TCAGTCCTGT AGAATCGACC TCTGCTGGCC GGCTGTACCC TGAGTACCCT	3650
	CTCACTTCCT CTTCAGGTT TTCAGGGGAC AGGCCAACCC AGAGGACAGG	3700

SUBSTITUTE SHEET (RULE 26)

5	ATTCCTGGA GGCCACAGAG GAGCACCAG GAGAAGATCT GTAAGTAGGC	3750
	CTTTGTTAGA GTCTCCAAGG TTCAGTTCTC AGCTGAGGCC TCTCACACAC	3800
	TCCCTCTCTC CCCAGGCCTG TGGGTCTTCA TTGCCAGCT CCTGCCACACA	3850
	CTCCTGCCTG CTGCCCTGAC GAGAGTCATC	3880
	ATG TCT CTT GAG CAG AGG AGT CTG CAC TGC AAG CCT GAG GAA	3922
10	GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG GTG TGT GTG	3964
	CAG GCT GCC ACC TCC TCC TCC TCT CCT CTG GTC CTG GGC ACC	4006
	CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT CCT CCC CAG	4048
	AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC ATC AAC TTC	4090
	ACT CGA CAG AGG CAA CCC AGT GAG GGT TCC AGC AGC CGT GAA	4132
15	GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG TCC TTG TTC	4174
	CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG GTT GGT TTT	4216
	CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC ACA AAG GCA	4258
	GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG CAC TGT TTT	4300
	CCT GAG ATC TTC GGC AAA GCC TCT GAG TCC TTG CAG CTG GTC	4342
20	TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC GGC CAC TCC	4384
	TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT GAT GGC CTG	4426
	CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC TTC CTG ATA	4468
	ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC GGC CAT GCT CCT	4510
	GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG GAG GTG TAT	4552
25	GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC AGG AAG CTG	4594
	CTC ACC CAA GAT TTG GTG CAG GAA AAG TAC CTG GAG TAC GGC	4636
	AGG TGC CGG ACA GTG ATC CCG CAC GCT ATG AGT TCC TGT GGG	4678
	GTC CAA GGG CCC TCG CTG AAA CCA GCT ATG TGA	4711
	AAGTCCTTGA GTATGTGATC AAGGTCAGTG CAAGAGTTC	4750
30	GCTTTTTCTT CCCATCCCTG CGTGAAGCAG CTTTGAGAGA GGAGGAAGAG	4800
	GGAGTCTGAG CATGAGTTGC AGCCAAGGCC AGTGGGAGGG GGAAGTGGCC	4850
	AGTGCACCTT CCAGGGCCGC GTCCAGCAGC TTCCCTGCC TCGTGTGACA	4900
	TGAGGCCCAT TCTTCACTCT GAAGAGAGCG GTCAGTGTTT TCAGTAGTAG	4950
	GTTTCTGTTT TATTGGGTGA CTTGGAGATT TATCTTTGTT CTCTTTTGGA	5000
35	ATTGTTCAAA TGTTTTTTTT TAAGGGATGG TTGAATGAAC TTCAGCATCC	5050
	AAGTTTATGA ATGACAGCAG TCACACAGTT CTGTGTATAT AGTTTAAGGG	5100
	TAAGAGTCTT GTGTTTTATT CAGATTGGGA AATCCATTCT ATTTTGTGAA	5150
	TTGGGATAAT AACAGCAGTG GAATAAGTAC TTAGAAATGT GAAAAATGAG	5200
	CAGTAAATA GATGAGATAA AGAACTAAAG AAATTAAGAG ATAGTCAATT	5250
40	CTTGCCATTAT ACCTCAGTCT ATTCTGTAAA ATTTTAAAG ATATATGCAT	5300
	ACCTGGATTT CCTTGGCTTC TTTGAGAATG TAAGAGAAAT TAAATCTGAA	5350

SUBSTITUTE SHEET (RULE 26)

31

5	TAAAGAATTC TTCCTGTTCA CTGGCTCTTT TCTTCTCCAT GCACTGAGCA	5400
	TCTGCTTTTT GGAAGGCCCT GGGTTAGTAG TGGAGATGCT AAGGTAAGCC	5450
	AGACTCATAC CCACCCATAG GGTCGTAGAG TCTAGGAGCT GCAGTCACGT	5500
	AATCGAGGTG GCAAGATGTC CTCTAAAGAT GTAGGGAAAA GTGAGAGAGG	5550
	GGTGAGGGTG TGGGGCTCCG GGTGAGAGTG GTGGAGTGTC AATGCCCTGA	5600
10	GCTGGGGCAT TTTGGGCTTT GGGAAACTGC AGTTCCTTCT GGGGGAGCTG	5650
	ATTGTAATGA TCTTGGGTGG ATCC	5674

(2) INFORMATION FOR SEQUENCE ID NO: 9:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 4157 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
20	(ii) MOLECULE TYPE: genomic DNA
	(ix) FEATURE:
	(A) NAME/KEY: MAGE-2 gene
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

25	CCCATCCAGA TCCCCATCCG GGCAGAATCC GGTTCACCCC TTGCCGTGAA	50
	CCCAGGGAAG TCACGGGCCC GGATGTGACG CCACTGACTT GCACATTGGA	100
	GGTCAGAGGA CAGCGAGATT CTCGCCCTGA GCAACGGCCT GACGTCGGCG	150
	GAGGGAAGCA GGCGCAGGCT CCGTGAGGAG GCAAGGTAAG ACGCCGAGGG	200
30	AGGACTGAGG CGGGCCTCAC CCCAGACAGA GGGCCCCCAA TTAATCCAGC	250
	GCTGCCTCTG CTGCCGGGCC TGGACCACCC TGCAGGGGAA GACTTCTCAG	300
	GCTCAGTCGC CACCACCTCA CCCC GCCACC CCCC GCCGCT TTAACCGCAG	350
	GGA ACTCTGG CGTAAGAGCT TTGTGTGACC AGGGCAGGGC TGGTTAGAAG	400
	TGCTCAGGGC CCAGACTCAG CCAGGAATCA AGGTCAGGAC CCCAAGAGGG	450
35	GACTGAGGGC AACCACCCCC CTACCCTCAC TACCAATCCC ATCCCCCAAC	500
	ACCAACCCCA CCCCCATCCC TCAAACACCA ACCCCACCCC CAAACCCCAT	550
	TCCCATCTCC TCCCCACCA CCATCCTGGC AGAATCCGGC TTTGCCCTG	600
	CAATCAACCC ACGGAAGCTC CGGGAATGGC GGCCAAGCAC GCGGATCCTG	650
	ACGTTACAT GTACGGCTAA GGGAGGGAAG GGGTTGGGTC TCGTGAGTAT	700
40	GGCCTTTGGG ATGCAGAGGA AGGGCCCAGG CCTCCTGGAA GACAGTGGAG	750
	TCCTTAGGGG ACCCAGCATG CCAGGACAGG GGGCCCACTG TACCCTGTC	800

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5	TCAAAC TGAG CCACCTTTTC ATTCAGCCGA GGGAATCCTA GGGATGCAGA	850
	CCCAC TTCAG GGGGTTGGGG CCCAGCCTGC GAGGAGTCAA GGGGAGGAAG	900
	AAGAGGGAGG ACTGAGGGGA CCTTGGAGTC CAGATCAGTG GCAACCTTGG	950
	GCTGGGGGAT CCTGGGCACA GTGGCCGAAT GTGCCCCGTG CTCATTGCAC	1000
	CTTCAGGGTG ACAGAGAGTT GAGGGCTGTG GTCTGAGGGC TGGGACTTCA	1050
10	GGTCAGCAGA GGGAGGAATC CCAGGATCTG CCGGACCCAA GGTGTGCCCC	1100
	CTTCATGAGG ACTCCCCATA CCCCCGGCCC AGAAAGAAGG GATGCCACAG	1150
	AGTCTGGAAG TAAATTGTTC TTAGCTCTGG GGGAACCTGA TCAGGGATGG	1200
	CCCTAAGTGA CAATCTCATT TGTACCACAG GCAGGAGGTT GGGGAACCCT	1250
	CAGGGAGATA AGGTGTTGGT GTAAAGAGGA GCTGTCTGCT CATTT CAGGG	1300
15	GGTTCCCCCT TGAGAAAGGG CAGTCCCTGG CAGGAGTAA GATGAGTAAC	1350
	CCACAGGAGG CCATCATAAC GTTCACCCTA GAACCAAAGG GGTCAGCCCT	1400
	GGACAACGCA CGTGGGGTAA CAGGATGTGG CCCCTCCTCA CTTGTCTTTC	1450
	CAGATCTCAG GGAGTTGATG ACCTTGTTTT CAGAAGGTGA CTCAGTCAAC	1500
	ACAGGGGCCC CTCTGGTCGA CAGATGCAGT GGTTCTAGGA TCTGCCAAGC	1550
20	ATCCAGGTGG AGAGCCTGAG GTAGGATTGA GGGTACCCCT GGGCCAGAAT	1600
	GCAGCAAGGG GGCCCCATAG AAATCTGCCC TGCCCCCTGCG GTTACTTCAG	1650
	AGACCCTGGG CAGGGCTGTC AGCTGAAGTC CCTCCATTAT CTGGGATCTT	1700
	TGATGTCAGG GAAGGGGAGG CCTTGGTCTG AAGGGGCTGG AGTCAGGTCA	1750
	GTAGAGGGAG GGTCTCAGGC CCTGCCAGGA GTGGACGTGA GGACCAAGCG	1800
25	GA CTCGTCAC CCAGGACACC TGGACTCAA TGAATTTGAC ATCTCTCGTT	1850
	GTCTTTCGCG GAGGACCTGG TCACGTATGG CCAGATGTGG GTCCCCCTCA	1900
	TCTCCTTCTG TACCATATCA GGGATGTGAG TTCTTGACAT GAGAGATTCT	1950
	CAAGCCAGCA AAAGGGTGGG ATTAGGCCCT ACAAGGAGAA AGGTGAGGGC	2000
	CCTGAGTGAG CACAGAGGGG ACCCTCCACC CAAGTAGAGT GGGGACCTCA	2050
30	CGGAGTCTGG CCAACCCTGC TGAGACTTCT GGGAATCCGT GGCTGTGCTT	2100
	GCAGTCTGCA CACTGAAGGC CCGTGCAATC CTCTCCAGG AATCAGGAGC	2150
	TCCAGGAACC AGGCAGTGAG GCCTTGGTCT GAGTCAGTGC CTCAGGTCAC	2200
	AGAGCAGAGG GGACGCAGAC AGTGCCAACA CTGAAGGTTT GCCTGGAATG	2250
	CACACCAAGG GCCCCACCCG CCCAGAACAA ATGGGACTCC AGAGGGCCTG	2300
35	GCCTCACCT CCCTATTCTC AGTCCTGCAG CCTGAGCATG TGCTGGCCGG	2350
	CTGTACCCTG AGGTGCCCTC CCACTTCCTC CTTCAGGTTC TGAGGGGGAC	2400
	AGGCTGACAA GTAGGACCCG AGGCACTGGA GGAGCATTGA AGGAGAAGAT	2450
	CTGTAAGTAA GCCTTTGTCA GAGCCTCCAA GGTT CAGTTC AGTTCTCACC	2500
	TAAGGCCTCA CACACGCTCC TTCTCTCCCC AGGCCTGTGG GTCTTCATTG	2550
40	CCCAGCTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCAG AGTCATC	2597
	ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA	2639

SUBSTITUTE SHEET (RULE 26)

5	GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG	2681
	CAG GCT CCT GCT ACT GAG GAG CAG CAG ACC GCT TCT TCC TCT	2723
	TCT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GCT GCC	2765
	GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC	2807
	TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT	2849
10	GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATG TTT	2891
	CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGG AAG	2933
	ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC	2975
	AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT GTC CTC	3017
	AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC	3059
15	TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA	3101
	GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG	3143
	GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG	3185
	CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA	3227
	ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	3269
20	CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GAC AGT GTC	3311
	TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG	3353
	GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT	3395
	GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA	3437
	ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT	3479
25	GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT	3521
	TTG AGA GAG GGA GAA GAG TGA	3542
	GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT	3592
	GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA	3642
	GGCCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG	3692
30	TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA	3742
	TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA	3792
	GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG	3842
	TAAGAGTCCT GTTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG	3892
	TTGTCACATA ATAACAGCAG TGAATATGT ATTTGCCTAT ATTGTGAACG	3942
35	AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT	3992
	TGCCTTATAC CTCAGTCTAT TATGTAAAT TAAAAATATG TGTATGTTTT	4042
	TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT	4092
	TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC	4142
	CCTGGTAGTA GTGGG	4157
40		

34

- 5 (2) INFORMATION FOR SEQUENCE ID NO: 10:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 10 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (ix) FEATURE:
- (A) NAME/KEY: MAGE-21 gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

15

	GGATCCCCAT GGATCCAGGA AGAATCCAGT TCCACCCCTG CTGTGAACCC	50
	AGGGAAGTCA CGGGGCCGGA TGTGACGCCA CTGACTTGCG CGTTGGAGGT	100
	CAGAGAACAG CGAGATTCTC GCCCTGAGCA ACGGCCTGAC GTCGGCGGAG	150
20	GGAAGCAGGC GCAGGCTCCG TGAGGAGGCA AGGTAAGATG CCGAGGGAGG	200
	ACTGAGGCGG GCCTCACCCC AGACAGAGGG CCCCCAATAA TCCAGCGCTG	250
	CCTCTGCTGC CAGGCCTGGA CCACCCTGCA GGGGAAGACT TCTCAGGCTC	300
	AGTCGCCACC ACCTCACCCC GCCACCCCCC GCCGCTTTAA CCGCAGGGAA	350
	CTCTGGTGTA AGAGCTTTGT GTGACCAGGG CAGGGCTGGT TAGAAGTGCT	400
25	CAGGGCCCAG ACTCAGCCAG GAATCAAGGT CAGGACCCCA AGAGGGGACT	450
	GAGGGTAACC CCCCCGCACC CCCACCACCA TTCCCATCCC CCAACACCAA	500
	CCCCACCCCC ATCCCCCAAC ACCAAACCCA CCACCATCGC TCAAACATCA	550
	ACGGCACCCC CAAACCCCGA TTCCCATCCC CACCCATCCT GGCAGAATCG	600
	GAGCTTTGCC CCTGCAATCA ACCCACGGAA GTCGGGGAA TGGCGGCCAA	650
30	GCACGCGGAT CC	662

(2) INFORMATION FOR SEQUENCE ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

40 (ix) FEATURE:

(A) NAME/KEY: cDNA MAGE-3

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5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

	GCCGCGAGGG AAGCCGGCCC AGGCTCGGTG AGGAGGCAAG GTTCTGAGGG	50
	GACAGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA	100
10	AGATCTGCCA GTGGGTCTCC ATTGCCCAGC TCCTGCCAC ACTCCCGCCT	150
	GTTGCCCTGA CCAGAGTCAT C	171
	ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA	213
	GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG	255
	CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT	297
15	TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC	339
	GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC	381
	CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT	423
	GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC	465
	CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG	507
20	GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC	549
	AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC	591
	GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT	633
	TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA	675
	GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG	717
25	GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG	759
	CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA	801
	AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	843
	CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG	885
	TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG	927
30	GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT	969
	GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA	1011
	ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT	1053
	GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT	1095
	TTG AGA GAG GGG GAA GAG TGA	1116
35	GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT	1166
	GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCTCC TGTGACGTGA	1216
	GGCCATTCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG	1266
	TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG	1316
	TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG	1366
40	GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG	1416
	TAAGAGTCTT GttTTTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA	1466

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5 TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC 1516
 GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG 1566
 ATTCTTGCCT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA 1616
 ACCAGGATTT CCTTGACTTC TTTG 1640

10

(2) INFORMATION FOR SEQUENCE ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 943 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-31 gene

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGATCCTCCA CCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCTT 50
 CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG 100
 25 GCCCGTGGAT TCCTCTCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG 150
 AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGgCTCA 200
 GATAGTGCCA ACGGTGAAGG TTTGCCCTTG ATTCAAACCA AGGGCCCCAC 250
 CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT 300
 TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC 350
 30 CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC 400
 AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG 450
 TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC 500
 TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCAGCT CCTGCCCCACA 550
 CTCCCGCTG TTGCCCTGAC CAGAGTCATC 580
 35 ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 622
 GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG 664
 CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT 706
 TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC 748
 GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 790
 40 CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT 832
 GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC 874

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5 CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG 916
 GTG GCC AAG TTG GTT CAT TTT CTG CTC 943

10 2) INFORMATION FOR SEQUENCE ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2531 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAG-4 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

20

	GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG	50
	GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC	100
	TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG	150
25	GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT	200
	TGGTCTGAGA CAGTGTCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT	250
	GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA	300
	CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT	350
	CCTGCAGAAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA	400
30	CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC	450
	TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT	500
	TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC	550
	TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACTCTTG	600
	CCTGCTGCCC TGACCAGAGT CATC	624
35	ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	666
	GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCA	708
	CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC	750
	TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT	792
	GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT	834
40	GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC	876
	AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC	918

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5	TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC	960
	AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA	1002
	GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC	1044
	ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA	1086
	GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG	1128
10	GAA GTG GAC CCC GCC AGC AAC ACC TAC ACC CTT GTC ACC TGC	1170
	CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC	1212
	TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT	1254
	GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG	1296
	GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT	1338
15	GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG	1380
	CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT	1422
	CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT	1464
	GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC	1506
	AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA	1548
20	GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA	1578
	GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC	1628
	ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC	1678
	CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT	1728
	TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT	1778
25	GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT	1828
	TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG	1878
	AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG	1928
	GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT	1978
	GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCCGCC TTATGCCTCA	2028
30	GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTCCTTGG	2078
	CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA	2128
	ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC	2178
	AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA	2228
	GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT	2278
35	CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT	2328
	GAGAGTGGTC GGGTGTAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA	2378
	AACTGCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC	2428
	AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC	2478
	TCTGAGCAGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT	2528
40	GGG	2531

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(2) INFORMATION FOR SEQUENCE ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2531 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

15

(A) NAME/KEY: MAGE-41 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

	GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG	50
20	GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC	100
	TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG	150
	GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT	200
	TGGTCTGAGA CAGTGTCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT	250
	GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA	300
25	CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT	350
	CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA	400
	CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC	450
	TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT	500
	TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC	550
30	TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACCTTG	600
	CCTGCTGCCC TGAGCAGAGT CATC	624
	ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	666
	GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCG	708
	CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC	750
35	TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT	792
	GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT	834
	GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC	876
	AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC	918
	TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC	960
40	AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA	1002
	GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC	1044

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5	ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA	1086
	GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG	1128
	GAA GTG GAC CCC ACC AGC AAC ACC TAC ACC CTT GTC ACC TGC	1170
	CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC	1212
	TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT	1254
10	GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG	1296
	GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT	1338
	GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG	1380
	CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT	1422
	CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT	1464
15	GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC	1506
	AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA	1548
	GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA	1578
	GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC	1628
	ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC	1678
20	CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT	1728
	TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT	1778
	GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT	1828
	TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG	1878
	AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG	1928
25	GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT	1978
	GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCTGCC TTATGCCTCA	2028
	GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCTTTGG	2078
	CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTGA	2128
	ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC	2178
30	AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA	2228
	GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT	2278
	CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT	2328
	GAGAGTGGTC GGGTGTAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA	2378
	AACTCCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC	2428
35	AGGGCCAGAT TCTCAGAGGG AGAGGGGAAA GCCCAGATTG GAAAAGTTGC	2478
	TCTGAGCGGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT	2528
	GGG	2531

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- 5 (2) INFORMATION FOR SEQUENCE ID NO: 15:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1068 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
10 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA to mRNA
(ix) FEATURE:
(A) NAME/KEY: cDNA MAGE-4
15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

5 G GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA 40
GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG 82
CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA 124
20 ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT 166
GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT 208
GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC 250
ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG 292
GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC 334
25 GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG 376
GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT 418
GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC 460
ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG 502
GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT 544
30 CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG 586
CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA 628
TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC 670
TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG 720
TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG 770
35 GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTT TTAGTAGTGG 820
GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA 870
ATTGTTGAAA TGTTCTTTT AATGGATGGT TGAATTAAT TCAGCATCCA 920
AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT 970
AAGAGTCTTG TTTTATTTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT 1020
40 TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC 1068

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5 (2) INFORMATION FOR SEQUENCE ID NO: 16:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 10 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-5 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

15
 GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG 50
 GGGACCATTG ACCCAAGAG GGTGGAGACC TCACAGATTG CAGCCTACCC 100
 TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCCTGAG 150
 GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT 200
 20 TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC 250
 TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC 300
 GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG 350
 TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT 400
 CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG 450
 25 GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG 500
 ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCACT TTTTAGCTGA 550
 GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC 600
 AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 644
 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 686
 30 CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG 728
 GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA 770
 TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA 812
 AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC 854
 CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG 896
 35 TGG CTG ACT TGA 908
 TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCTGGT CACAAAGGCA 958
 GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT 1008
 CTTGCGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA 1058
 AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA 1108
 40 CTCCTATGAT GGCCTGCTGG TTGATAATAA TCAGATCATG CCCAAGACGG 1158
 GCCTCCTGAT AATCGTCTTG GGCATGATTG CAATGGAGGG CAAATGCGTC 1208

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5	CCTGAGGAGA AAATCTGGGA GGAGCTGAGT GTGATGAAGG TGTATGTTGG	1258
	GAGGGAGCAC AGTGTCTGTG GGGAGCCCAG GAAGCTGCTC ACCCAAGATT	1308
	TGGTGCAGGA AAATACTG GAGTACCGGC AGGTGCCCAG CAGTGATCCC	1358
	ATATGCTATG AGTTACTGTG GGGTCCAAGG GCACTCGCTG CTTGAAAGTA	1408
	CTGGAGCACG TGGTCAGGGT CAATGCAAGA GTTCTCATTT CCTACCCATC	1458
10	CCTGCGTGAA GCAGCTTTGA GAGAGGAGGA AGAGGGAGTC TGAGCATGAG	1508
	CTGCAGCCAG GGCCACTGCG AGGGGGGCTG GGCCAGTGCA CCTTCCAGGG	1558
	CTCCGTCCAG TAGTTTCCCC TGCCTTAATG TGACATGAGG CCCATTCTTC	1608
	TCTCTTTGAA GAGAGCAGTC AACATTCTTA GTAGTGGGT TCTGTTCTAT	1658
	TGGATGACTT TGAGATTTGT CTTTGTTC TTTTGAATT GTTCAAATGT	1708
15	TTCTTTTAAT GGGTGGTTGA ATGAACTTCA GCATTCAAAT TTATGAATGA	1758
	CAGTAGTCAC ACATAGTGCT GTTTATATAG TTTAGGAGTA AGAGTCTTGT	1808
	TTTTTATTCA GATTGGGAAA TCCATTCCAT TTTGTGAATT GGGACATAGT	1858
	TACAGCAGTG GAATAAGTAT TCATTTAGAA ATGTGAATGA GCAGTAAAC	1908
	TGATGACATA AAGAAATTAA AAGATATTTA ATTCTTGCTT AACTCAGTC	1958
20	TATTCGGTAA AATTTTTTTT AAAAAATGTG CATACTGGA TTTCTTGGC	2008
	TTCTTTGAGA ATGTAAGACA AATTAAATCT GAATAAATCA TTCTCCCTGT	2058
	TCACTGGCTC ATTTATTCTC TATGCACTGA GCATTTGCTC TGTGGAAGGC	2108
	CCTGGGTAA TAGTGGAGAT GCTAAGGTAA GCCAGACTCA CCCCTACCCA	2158
	CAGGGTAGTA AAGTCTAGGA GCAGCAGTCA TATAATTAAG GTGGAGAGAT	2208
25	GCCCTCTAAG ATGTAGAG	2226

(2) INFORMATION FOR SEQUENCE ID NO: 17:

- | | |
|----|---|
| 30 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 2305 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: single |
| | (D) TOPOLOGY: linear |
| 35 | (ii) MOLECULE TYPE: genomic DNA |
| | (ix) FEATURE: |
| | (A) NAME/KEY: MAGE-51 gene |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17: |

40	GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG	50
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5	GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC	100
	TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG	150
	GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT	200
	TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC	250
	TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCATC	300
10	GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG	350
	TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT	400
	CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG	450
	GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG	500
	ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCACT TTTAGCTGA	550
15	GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC	600
	AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC	644
	ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	686
	GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC	728
	AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT	770
20	CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG	812
	GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA	854
	TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA	896
	AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC	938
	CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG	980
25	TGG CTG ACT TGA	992
	TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCCGGT CACAAAGGCA	1042
	GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT	1092
	CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA	1142
	AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA	1192
30	CTCCTATGAT GGCTGGTGG TTTAATCAGA TCATGCCCAA GACGGGCCTC	1242
	CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGGCAAAT GCGTCCCTGA	1292
	GGAGAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT GTTGGGAGGG	1342
	AGCACAGTGT CTGTGGGGAG CCCAGGAAGC TGCTCACCCA AGATTTGGTG	1392
	CAGGAAAACCT ACCTGGAGTA CCGCAGGTGC CCAGCAGTGA TCCCATATGC	1442
35	TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTTGAA AGTACTGGAG	1492
	CACGTGGTCA GGGTCAATGC AAGAGTTCTC ATTTCTACC CATCCCTGCA	1542
	TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCTGAGCA TGAGCTGCAG	1592
	CCAGGGCCAC TGCGAGGGGG GCTGGGCCAG TGCACCTTCC AGGGCTCCGT	1642
	CCAGTAGTTT CCCCTGCCTT AATGTGACAT GAGGCCCAT TTTCTCTCTT	1692
40	TGAAGAGAGC AGTCAACATT CTTAGTAGTG GGTTCCTGTT CTATTGGATG	1742
	ACTTTGAGAT TTGTCTTTGT TTCCTTTTGG AATTGTTCAA ATGTTCTTTT	1792

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5	TAATGGGTGG TTGAATGAAC TTCAGCATTC AAATTTATGA ATGACAGTAG	1842
	TCACACATAG TGCTGTTTAT ATAGTTTAGG AGTAAGAGTC TTGTTTTTTA	1892
	TTCAGATTGG GAAATCCATT CCATTTTGTG AATTGGGACA TAGTTACAGC	1942
	AGTGGAAATA GTATTCATTT AGAAATGTGA ATGAGCAGTA AACTGATGA	1992
	GATAAAGAAA TAAAAGATA TTTAATTCTT GCCTTATACT CAGTCTATTC	2042
10	GGTAAAATTT TTTTTTAAAA ATGTGCATAC CTGGATTTCCT TTGGCTTCTT	2092
	TGAGAATGTA AGACAAATTA AATCTGAATA AATCATTCTC CCTGTTCACT	2142
	GGCTCATTTA TTCTCTATGC ACTGAGCATT TGCTCTGTGG AAGGCCCTGG	2192
	GTTAATAGTG GAGATGCTAA GGTAAGCCAG ACTCACCCCT ACCCACAGGG	2242
	TAGTAAAGTC TAGGAGCAGC AGTCATATAA TTAAGGTGGA GAGATGCCCT	2292
15	CTAAGATGTA GAG	2305

(2) INFORMATION FOR SEQUENCE ID NO: 18:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- (A) NAME/KEY: MAGE-6 gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

30	TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG	42
	CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC	84
	GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC	126
	GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC	168
35	TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC	210
	TGT GCC CCT GAG GAG	225

- 40 (2) INFORMATION FOR SEQUENCE ID NO: 19:
- (i) SEQUENCE CHARACTERISTICS:

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5 (A) LENGTH: 1947 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 10 (ix) FEATURE:
 (A) NAME/KEY: MAGE-7 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

15	TGAATGGACA ACAAGGGCCC CACACTCCCC AGAACACAAG GGA	50
	GAGCCCAGCC TCACCTTCCC TACTGTCAGT CCTGCAGCCT CAGCCTCTGC	100
	TGGCCGGCTG TACCCTGAGG TGCCCTCTCA CTTCCCTCCTT CAGGTTCTCA	150
	GCGGACAGGC CGGCCAGGAG GTCAGAAGCC CCAGGAGGCC CCAGAGGAGC	200
	ACCGAAGGAG AAGATCTGTA AGTAGGCCTT TGTTAGGGCC TCCAGGGCGT	250
20	GGTTCACAAA TGAGGGCCCCT CACAAGCTCC TTCTCTCCCC AGATCTGTGG	300
	GTTCCCTCCCC ATCGCCCAGC TGCTGCCCCG ACTCCAGCCT GCTGCCCTGA	350
	CCAGAGTCAT CATGTCTTCT GAGCAGAGGA GTCAGCACTG CAAGCCTGAG	400
	GATGCCTTGA GGCCCAAGGA CAGGAGGCTC TGGGCCTGGT GGGTGCGCAG	450
	GCTCCCGCCA CCGAGGAGCA CGAGGCTGCC TCCTCCTTCA CTCTGATTGA	500
25	AGGCACCCTG GAGGAGGTGC CTGCTGCTGG GTCCCCCAGT CCTCCCTGA	550
	GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC ACTCTATGGA	600
	GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGAGGG GCCAACCACC	650
	TAGACACACC CCGCTCACCT GCGTCCTTG TTCCA	685
	ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC TGC ACA AGT	727
30	ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA TGC TGG ACA	769
	GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT GTG ATC TAT	811
	GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT GGC ATT GAC	853
	ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG TCC TTG TCA	895
	CCT GCT TGG GCC TCT CCT ACA ATG GCC TGC TGG GTG ATG ATC	937
35	AGA GCA TGC CCG AGA CCG GCC TTC TGA	964
	TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC CCCTGAGGAG	1014
	GCAATCTGGG AAGCGTTGAG TGTAATGGTG TATGATGGGA TGGAGCAGTT	1064
	TCTTTGGGCA GCTGAGGAAG CTGCTACCCC AAGATTGGGT GCAGGAAAAC	1114
	TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCCGT GCTACCAGTT	1164
40	CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG AAAGTCCTGG	1214
	AGTATGCAGC CAGGGTCAGT ACTAAAGAGA GCATTTCTTA CCCATCCCTG	1264

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5	CATGAAGAGG CTTTGGGAGA GGAGGAAGAG GGAGTCTGAG CAGAAGTTGC	1314
	AGCCAGGGCC AGTGGGGCAG ATTGGGGGAG GGCCTGGGCA GTGCACGTTC	1364
	CACACATCCA CCACCTTCCC TGTCTGTGA CATGAGGCCC ATTCTTCACT	1414
	CTGTGTTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGGG AGTGTGTTGG	1464
	GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCCTGT TCTCTTGGGC	1514
10	GATTTGGAGG TTTATCTTTG TTTCTTTTG CAGTCGTTCA AATGTTCTT	1564
	TTAATGGATG GTGTAATGAA CTTCAACATT CATTTCATGT ATGACAGTAG	1614
	GCAGACTTAC TGTTTTTTAT ATAGTTAAAA GTAAGTGCAT TGTTTTTTAT	1664
	TTATGTAAGA AAATCTATGT TATTTCTTGA ATTGGGACAA CATAACATAG	1714
	CAGAGGATTA AGTACCTTTT ATAATGTGAA AGAACAAAGC GGTAAAATGG	1764
15	GTGAGATAAA GAAATAAAGA AATTAAATTG GCTGGGCACG GTGGCTCACG	1814
	CCTGTAATCC CAGCACTTTA GGAGGCAGAG GCACGGGGAT CACGAGGTCA	1864
	GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT CTCTATTAAA	1914
	AATACAAAAC TTAGCCGGGC GTGGTGGCGG GTG	1947

20

(2) INFORMATION FOR SEQUENCE ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1810 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-8 gene

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

	GAGCTCCAGG AACCAGGCTG TGAGGTCTTG GTCTGAGGCA GTATCTTCAA	50
	TCACAGAGCA TAAGAGGCCC AGGCAGTAGT AGCAGTCAAG CTGAGGTGGT	100
	GTTTCCCCTG TATGTATACC AGAGGCCCTT CTGGCATCAG AACAGCAGGA	150
35	ACCCACAGT TCCTGGCCCT ACCAGCCCTT TTGTCAGTCC TGGAGCCTTG	200
	GCCTTTGCCA GGAGGCTGCA CCCTGAGATG CCCTCTCAAT TTCTCCTTCA	250
	GGTTGCGAGA GAACAGGCCA GCCAGGAGGT CAGGAGGCCC CAGAGAAGCA	300
	CTGAAGAAGA CCTGTAAGTA GACCTTTGTT AGGGCATCCA GGGTGTAGTA	350
	CCCAGCTGAG GCCTCTCACA CGCTTCCTCT CTCCCAGGC CTGTGGGTCT	400
40	CAATTGCCCA GCTCCGGCCC ACACTCTCCT GCTGCCCTGA CCTGAGTCAT	450
	C	451

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5	ATG CTT CTT GGG CAG AAG AGT CAG CGC TAC AAG GCT GAG GAA	493
	GGC CTT CAG GCC CAA GGA GAG GCA CCA GGG CTT ATG GAT GTG	535
	CAG ATT CCC ACA GCT GAG GAG CAG AAG GCT GCA TCC TCC TCC	577
	TCT ACT CTG ATC ATG GGA ACC CTT GAG GAG GTG ACT GAT TCT	619
	GGG TCA CCA AGT CCT CCC CAG AGT CCT GAG GGT GCC TCC TCT	661
10	TCC CTG ACT GTC ACC GAC AGC ACT CTG TGG AGC CAA TCC GAT	703
	GAG GGT TCC AGC AGC AAT GAA GAG GAG GGG CCA AGC ACC TCC	745
	CCG GAC CCA GCT CAC CTG GAG TCC CTG TTC CGG GAA GCA CTT	787
	GAT GAG AAA GTG GCT GAG TTA GTT CGT TTC CTG CTC CGC AAA	829
	TAT CAA ATT AAG GAG CCG GTC ACA AAG GCA GAA ATG CTT GAG	871
15	AGT GTC ATC AAA AAT TAC AAG AAC CAC TTT CCT GAT ATC TTC	913
	AGC AAA GCC TCT GAG TGC ATG CAG GTG ATC TTT GGC ATT GAT	955
	GTG AAG GAA GTG GAC CCT GCC GGC CAC TCC TAC ATC CTT GTC	997
	ACC TGC CTG GGC CTC TCC TAT GAT GGC CTG CTG GGT GAT GAT	1039
	CAG AGT ACG CCC AAG ACC GGC CTC CTG ATA ATC GTC CTG GGC	1081
20	ATG ATC TTA ATG GAG GGC AGC CGC GCC CCG GAG GAG GCA ATC	1123
	TGG GAA GCA TTG AGT GTG ATG GGG GCT GTA TGA	1156
	TGGGAGGGAG CACAGTGTCT ATTGGAAGCT CAGGAAGCTG CTCACCCAAG	1206
	AGTGGGTGCA GGAGAACTAC CTGGAGTACC GCCAGGCGCC CGGCAGTGAT	1256
	CCTGTGCGCT ACGAGTTCCT GTGGGGTCCA AGGGCCCTTG CTGAAACCAG	1306
25	CTATGTGAAA GTCCTGGAGC ATGTGGTCAG GGTCAATGCA AGAGTTCGCA	1356
	TTTCCTACCC ATCCCTGCAT GAAGAGGCTT TGGGAGAGGA GAAAGGAGTT	1406
	TGAGCAGGAG TTGCAGCTAG GGCCAGTGGG GCAGGTTGTG GGAGGGCCTG	1456
	GGCCAGTGCA CGTTCCAGGG CCACATCCAC CACTTTCCT GCTCTGTTAC	1506
	ATGAGGCCCA TTCTTCACTC TGTGTTTGAA GAGAGCAGTC ACAGTTCTCA	1556
30	GTAGTGGGGA GCATGTTGGG TGTGAGGGAA CACAGTGTGG ACCATCTCTC	1606
	AGTTCCTGTT CTATTGGGCG ATTTGGAGGT TTATCTTTGT TTCCTTTTGG	1656
	AATTGTTCCA ATGTTCTTC TAATGGATGG TGTAATGAAC TTCAACATTC	1706
	ATTTTATGTA TGACAGTAGA CAGACTTACT GCTTTTATA TAGTTTAGGA	1756
	GTAAGAGTCT TGCTTTTCAT TTATACTGGG AAACCCATGT TATTTCTTGA	1806
35	ATTC	1810

(2) INFORMATION FOR SEQUENCE ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 1412 base pairs

(B) TYPE: nucleic acid

49

- 5 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-9 gene
 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

	TCTGAGACAG TGTCTCAGG TCGCAGAGCA GAGGAGACCC AGGCAGTGTC	50
	AGCAGTGAAG GTGAAGTGTT CACCCTGAAT GTGCACCAAG GGCCCCACCT	100
	GCCCCAGCAC ACATGGGACC CCATAGCACC TGGCCCCATT CCCCCTACTG	150
15	TCACTCATAG AGCCTTGATC TCTGCAGGCT AGCTGCACGC TGAGTAGCCC	200
	TCTCACTTCC TCCCTCAGGT TCTCGGGACA GGCTAACCAG GAGGACAGGA	250
	GCCCCAAGAG GCCCCAGAGC AGCACTGACG AAGACCTGTA AGTCAGCCTT	300
	TGTTAGAACC TCCAAGGTTT GGTTCCTCAGC TGAAGTCTCT CACACACTCC	350
	CTCTCTCCCC AGGCCTGTGG GTCTCCATCG CCCAGCTCCT GCCACGCTC	400
20	CTGACTGCTG CCCTGACCAG AGTCATC	427
	ATG TCT CTC GAG CAG AGG AGT CCG CAC TGC AAG CCT GAT GAA	469
	GAC CTT GAA GCC CAA GGA GAG GAC TTG GGC CTG ATG GGT GCA	511
	CAG GAA CCC ACA GGC GAG GAG GAG GAG ACT ACC TCC TCC TCT	553
	GAC AGC AAG GAG GAG GAG GTG TCT GCT GCT GGG TCA TCA AGT	595
25	CCT CCC CAG AGT CCT CAG GGA GGC GCT TCC TCC TCC ATT TCC	637
	GTC TAC TAC ACT TTA TGG AGC CAA TTC GAT GAG GGC TCC AGC	679
	AGT CAA GAA GAG GAA GAG CCA AGC TCC TCG GTC GAC CCA GCT	721
	CAG CTG GAG TTC ATG TTC CAA GAA GCA CTG AAA TTG AAG GTG	763
	GCT GAG TTG GTT CAT TTC CTG CTC CAC AAA TAT CGA GTC AAG	805
30	GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGC GTC ATC AAA	847
	AAT TAC AAG CGC TAC TTT CCT GTG ATC TTC GGC AAA GCC TCC	889
	GAG TTC ATG CAG GTG ATC TTT GGC ACT GAT GTG AAG GAG GTG	931
	GAC CCC GCC GGC CAC TCC TAC ATC CTT GTC ACT GCT CTT GGC	973
	CTC TCG TGC GAT AGC ATG CTG GGT GAT GGT CAT AGC ATG CCC	1015
35	AAG GCC GCC CTC CTG ATC ATT GTC CTG GGT GTG ATC CTA ACC	1057
	AAA GAC AAC TGC GCC CCT GAA GAG GTT ATC TGG GAA GCG TTG	1099
	AGT GTG ATG GGG GTG TAT GTT GGG AAG GAG CAC ATG TTC TAC	1141
	GGG GAG CCC AGG AAG CTG CTC ACC CAA GAT TGG GTG CAG GAA	1183
	AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCG	1225
40	CAC TAC GAG TTC CTG TGG GGT TCC AAG GCC CAC GCT GAA ACC	1267
	AGC TAT GAG AAG GTC ATA AAT TAT TTG GTC ATG CTC AAT GCA	1309

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5 AGA GAG CCC ATC TGC TAC CCA TCC CTT TAT GAA GAG GTT TTG 1351
 GGA GAG GAG CAA GAG GGA GTC TGA 1375
 GCACCAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTCA 1412

10 (2) INFORMATION FOR SEQUENCE ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 920 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-10 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

20

ACCTGCTCCA GGACAAAGTG GACCCCACTG CATCAGCTCC ACCTACCCTA 50
 CTGTCAGTCC TGGAGCCTTG GCCTCTGCCG GCTGCATCCT GAGGAGCCAT 100
 CTCTCACTTC CTTCTTCAGG TTCTCAGGGG ACAGGGGAGAG CAAGAGGTCA 150
 25 AGAGCTGTGG GACACCACAG AGCAGCACTG AAGGAGAAGA CCTGTAAGTT 200
 GGCCTTTGTT AGAACCTCCA GGGTGTGGTT CTCAGCTGTG GCCACTTACA 250
 CCCTCCCTCT CTCCCCAGGC CTGTGGGTCC CCATCGCCCA AGTCCTGCCC 300
 ACACTCCAC CTGCTACCCT GATCAGAGTC ATC 333
 ATG CCT CGA GCT CCA AAG CGT CAG CGC TGC ATG CCT GAA GAA 375
 30 GAT CTT CAA TCC CAA AGT GAG ACA CAG GGC CTC GAG GGT GCA 417
 CAG GCT CCC CTG GCT GTG GAG GAG GAT GCT TCA TCA TCC ACT 459
 TCC ACC AGC TCC TCT TTT CCA TCC TCT TTT CCC TCC TCC TCC 501
 TCT TCC TCC TCC TCC TCC TGC TAT CCT CTA ATA CCA AGC ACC 543
 CCA GAG GAG GTT TCT GCT GAT GAT GAG ACA CCA AAT CCT CCC 585
 35 CAG AGT GCT CAG ATA GCC TGC TCC TCC CCC TCG GTC GTT GCT 627
 TCC CTT CCA TTA GAT CAA TCT GAT GAG GGC TCC AGC AGC CAA 669
 AAG GAG GAG AGT CCA AGC ACC CTA CAG GTC CTG CCA GAC AGT 711
 GAG TCT TTA CCC AGA AGT GAG ATA GAT GAA AAG GTG ACT GAT 753
 TTG GTG CAG TTT CTG CTC TTC AAG TAT CAA ATG AAG GAG CCG 795
 40 ATC ACA AAG GCA GAA ATA CTG GAG AGT GTC ATA AAA AAT TAT 837
 GAA GAC CAC TTC CCT TTG TTG TTT AGT GAA GCC TCC GAG TGC 879

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5 ATG CTG CTG GTC TTT GGC ATT GAT GTA AAG GAA GTG GAT CC 920

(2) INFORMATION FOR SEQUENCE ID NO: 23:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 15 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-11 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

20 AGAGAACAGG CCAACCTGGA GGACAGGAGT CCCAGGAGAA CCCAGAGGAT 50
 CACTGGAGGA GAACAAGTGT AAGTAGGCCT TTGTTAGATT CTCCATGGTT 100
 CATATCTCAT CTGAGTCTGT TCTACGCTC CCTCTCTCCC CAGGCTGTGG 150
 GGCCCCATCA CCCAGATATT TCCCACAGTT CGGCCTGCTG ACCTAACCAG 200
 25 AGTCATCATG CCTCTTGAGC AAAGAAGTCA GCACTGCAAG CCTGAGGAAG 250
 CCTTCAGGCC CAAGAAGAAG ACCTGGGCCT GGTGGGTGCA CAGGCTCTCC 300
 AAGCTGAGGA GCAGGAGGCT GCCTTCTTCT CCTTACTCT GAATGTGGGC 350
 ACTCTAGAGG AGTTGCCTGC TGCTGAGTCA CCAAGTCCTC CCCAGAGTCC 400
 TCAGGAAGAG TCCTTCTCTC CCACTGCCAT GGATGCCATC TTTGGGAGCC 450
 30 TATCTGATGA GGGCTCTGGC AGCCAAGAAA AGGAGGGGCC AAGTACCTCG 500
 CCTGACCTGA TAGACCCTGA GTCCTTTTCC CAAGATATAC TACATGACAA 550
 GATAATTGAT TTGGTTTATT TATTCTCCGC AAGTATCGAG TCAAGGGGCT 600
 GATCACAAAG GCAGAA 616
 ATG CTG GGG AGT GTC ATC AAA AAT TAT GAG GAC TAC TTT CCT 658
 35 GAG ATA TTT AGG GAA GCC TCT GTA TGC ATG CAA CTG CTC TTT 700
 GGC ATT GAT GTG AAG GAA GTG GAC CCC ACT AGC CAC TCC TAT 742
 GTC CTT GTC ACC TCC CTC AAC CTC TCT TAT GAT GGC ATA CAG 784
 TGT AAT GAG CAG AGC ATG CCC AAG TCT GGC CTC CTG ATA ATA 826
 GTC CTG GGT GTA ATC TTC ATG GAG GGG AAC TGC ATC CCT GAA 868
 40 GAG GTT ATG TGG GAA GTC CTG AGC ATT ATG GGG GTG TAT GCT 910
 GGA AGG GAG CAC TTC CTC TTT GGG GAG CCC AAG AGG CTC CTT 952

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5 ACC CAA AAT TGG GTG CAG GAA AAG TAC CTG GTG TAC CGG CAG 994
 GTG CCC GGC ACT GAT CCT GCA TGC TAT GAG TTC CTG TGG GGT 1036
 CCA AGG GCC CAC GCT GAG ACC AGC AAG ATG AAA GTT CTT GAG 1078
 TAC ATA GCC AAT GCC AAT GGG AGG GAT CC 1107

10

(2) INFORMATION FOR SEQUENCE ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2150 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: smage-I

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TCTGTCTGCA TATGCCTCCA CTTGTGTGTA GCAGTCTCAA ATGGATCTCT 50
 CTCTACAGAC CTCTGTCTGT GTCTGGCACC CTAAGTGGCT TTGCATGGGC 100
 25 ACAGGTTTCT GCCCCTGCAT GGAGCTTAAA TAGATCTTTC TCCACAGGCC 150
 TATACCCCTG CATTGTAAGT TTAAGTGGCT TTATGTGGAT ACAGGTCTCT 200
 GCCCTTGTAT GCAGGCCTAA GTTTTTCTGT CTGCTTAACC CCTCCAAGTG 250
 AAGCTAGTGA AAGATCTAAC CCACTTTTGG AAGTCTGAAA CTAGACTTTT 300
 ATGCAGTGGC CTAACAAGTT TTAATTTCTT CCACAGGGTT TGCAGAAAAG 350
 30 AGCTTGATCC ACGAGTTCAG AAGTCCTGGT ATGTTCTTAG AAAG 394
 ATG TTC TCC TGG AAA GCT TCA AAA GCC AGG TCT CCA TTA AGT 436
 CCA AGG TAT TCT CTA CCT GGT AGT ACA GAG GTA CTT ACA GGT 478
 TGT CAT TCT TAT CCT TCC AGA TTC CTG TCT GCC AGC TCT TTT 520
 ACT TCA GCC CTG AGC ACA GTC AAC ATG CCT AGG GGT CAA AAG 562
 35 AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG CAG TCA CGC AGG 604
 GAG GTT CCA GTA GTT CAG CCC ACT GCA GAG GAA GCA GGG TCT 646
 TCT CCT GTT GAC CAG AGT GCT GGG TCC AGC TTC CCT GGT GGT 688
 TCT GCT CCT CAG GGT GTG AAA ACC CCT GGA TCT TTT GGT GCA 730
 GGT GTA TCC TGC ACA GGC TCT GGT ATA GGT GGT AGA AAT GCT 772
 40 GCT GTC CTG CCT GAT ACA AAA AGT TCA GAT GGC ACC CAG GCA 814
 GGG ACT TCC ATT CAG CAC ACA CTG AAA GAT CCT ATC ATG AGG 856

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5	AAG GCT AGT GTG CTG ATA GAA TTC CTG CTA GAT AAA TTT AAG	898
	ATG AAA GAA GCA GTT ACA AGG AGT GAA ATG CTG GCA GTA GTT	940
	AAC AAG AAG TAT AAG GAG CAA TTC CCT GAG ATC CTC AGG AGA	982
	ACT TCT GCA CGC CTA GAA TTA GTC TTT GGT CTT GAG TTG AAG	1024
	GAA ATT GAT CCC AGC ACT CAT TCC TAT TTG CTG GTA GGC AAA	1066
10	CTG GGT CTT TCC ACT GAG GGA AGT TTG AGT AGT AAC TGG GGG	1108
	TTG CCT AGG ACA GGT CTC CTA ATG TCT GTC CTA GGT GTG ATC	1150
	TTC ATG AAG GGT AAC CGT GCC ACT GAG CAA GAG GTC TGG CAA	1192
	TTT CTG CAT GGA GTG GGG GTA TAT GCT GGG AAG AAG CAC TTG	1234
	ATC TTT GGC GAG CCT GAG GAG TTT ATA AGA GAT GTA GTG CGG	1276
15	GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT GGC AGT GAT CCC	1318
	CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA GCC CAT GCT GAA	1360
	ACA ACC AAG ATG AAA GTC CTG GAA GTT TTA GCT AAA GTC AAT	1402
	GGC ACA GTC CCT AGT GCC TTC CCT AAT CTC TAC CAG TTG GCT	1444
	CTT AGA GAT CAG GCA GGA GGG GTG CCA AGA AGG AGA GTT CAA	1486
20	GGC AAG GGT GTT CAT TCC AAG GCC CCA TCC CAA AAG TCC TCT	1528
	AAC ATG TAG	1537
	TTGAGTCTGT TCTGTTGTGT TTGAAAAACA GTCAGGCTCC TAATCAGTAG	1587
	AGAGTTCATA GCCTACCAGA ACCAACATGC ATCCATTCTT GGCCTGTTAT	1637
	ACATTAGTAG AATGGAGGCT ATTTTGTGTA CTTTCAAAT GTTTGTTTAA	1687
25	CTAAACAGTG CTTTTTGCCA TGCTTCTTGT TAACTGCATA AAGAGGTAAC	1737
	TGTCAC TTGT CAGATTAGGA CTGTGTTTGT TATTTGCAAC AAAC TGGAAA	1787
	ACATTATTTT GTTTTACTA AAACATTGTG TAACATTGCA TTGGAGAAGG	1837
	GATTGTCATG GCAATGTGAT ATCATACAGT GGTGAAACAA CAGTGAAGTG	1887
	GGAAAGTTTA TATTGTAAAT TTTGAAAATT TTATGAGTGT GATTGCTGTA	1937
30	TACTTTTTTC TTTTTGTAT AATGCTAAGT GAAATAAAGT TGGATTTGAT	1987
	GACTTTACTC AAATTCATTA GAAAGTAAAT CGTAAACTC TATTACTTTA	2037
	TTATTTTCTT CAATTATGAA TTAAGCATTG GTTATCTGGA AGTTTCTCCA	2087
	GTAGCACAGG ATCTAGTATG AAATGTATCT AGTATAGGCA CTGACAGTGA	2137
	GTTATCAGAG TCT	2150

35

(2) INFORMATION FOR SEQUENCE ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2099 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

40

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5. (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(ix) FEATURE:
(A) NAME/KEY: smage-II
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

10

	ACCTTATTGG GTCTGTCTGC ATATGCCTCC ACTTGTGTGT AGCAGTCTCA	50
	AATGGATCTC TCTCTACAGA CCTCTGTCTG TGTCTGGCAC CCTAAGTGGC	100
	TTTGCATGGG CACAGGTTTC TGCCCTGCA TGGAGCTTAA ATAGATCTTT	150
15	CTCCACAGGC CTATACCCCT GCATTGTAAG TTTAAGTGGC TTTATGTGGA	200
	TACAGGTCTC TGCCCTTGTA TGCAGGCCTA AGTTTTTCTG TCTGCTTAGC	250
	CCCTCCAAGT GAAGCTAGTG AAAGATCTAA CCCACTTTTG GAAGTCTGAA	300
	ACTAGACTTT TATGCAGTGG CCTAACAAGT TTTAATTTCT TCCACAGGGT	350
	TTGCAGAAAA GAGCTTGATC CACGAGTTCG GAAGTCCTGG TATGTTCTTA	400
20	GAAAGATGTT CTCCTGGAAG GCTTCAAAAG CCAGGTCTCC ATTAAGTCCA	450
	AGGTATTCTC TACCTGGTAG TACAGAGGTA CTTACAGGTT GTCATTCTTA	500
	TCTTTCCAGA TTCCTGTCTG CCAGCTCTTT TACTTCAGCC CTGAGCACAG	550
	TCAACATGCC TAGGGGTCAA AAGAGTAAGA CCCGCTCCCG TGCAAAACGA	600
	CAGCAGTCAC GCAGGGAGGT TCCAGTAGTT CAGCCCCTG CAGAGGAAGC	650
25	AGGGTCTTCT CCTGTTGACC AGAGTGCTGG GTCCAGCTTC CCTGGTGGTT	700
	CTGCTCCTCA GGGTGTGAAA ACCCCTGGAT CTTTTGGTGC AGGTGTATCC	750
	TGCACAGGCT CTGGTATAGG TGGTAGAAAT GCTGCTGTCC TGCCTGATAC	800
	AAAAAGTTCA GATGGCACCC AGGCAGGGAC TTCCATTGAG CACACACTGA	850
	AAGATCCTAT CATGAGGAAG GCTAGTGTGC TGATAGAATT CCTGCTAGAT	900
30	AAGTTTAAGA TGAAAGAAGC AGTTACAAGG AGTGAAATGC TGGCAGTAGT	950
	TAACAAGAAG TATAAGGAGC AATTCCTGTA GATCCTCAGG AGAACTTCTG	1000
	CACGCCTAGA ATTAGTCTTT GGTCTTGAGT TGAAGGAAAT TGATCCCAGC	1050
	ACTCATTCTT ATTTGCTGGT AGGCAAACTG GGTCTTTCCA CTGAGGGAAG	1100
	TTTGAGTAGT AACTGGGGGT TGCCTAGGAC AGGTCTCCTA ATGTCTGTCC	1150
35	TAGGTGTGAT CTTGATGAAG GGTAACCGTG CCACTGAGCA AGAGGTCTGG	1200
	CAATTTCTGC ATGGAGTGGG GGTATATGCT GGGGAAGAAGC ACTTGATCTT	1250
	TGGCGAGCCT GAGGAGTTTA TAAGAGATGT AGTGCGGGAA AATTACCTGG	1300
	AGTACCGCCA GGTACCTGGC AGTGATCCCC CAAGCTATGA GTTCCTGTGG	1350
	GGACCCAGAG CCCATGCTGA AACAACCAAG ATGAAAGTCC TGGAAGTTTT	1400
40	AGCTAAAGTC AATGGCACAG TCCCTAGTGC CTTCCCTAAT CTCTACCAGT	1450
	TGGCTCTTAG AGATCAGGCA GGAGGGGTGC CAAGAAGGAG AGTTCAAGGC	1500

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55

5 AAGGGTG TTC ATTCCAAGGC CCCATCCCAA AAGTCCTCTA ACATGTAGTT 1550
GAGTCTG TTC TGTTGTG TTT GAAAAACAGT CAGGCTCCTA ATCAGTAGAG 1600
AGTTCATAGC CTACCAGAAC CAACATGCAT CCATTCTTGG CCTGTTATAC 1650
ATTAGTAGAA TGGAGGCTAT TTTTGTTACT TTTCAAATGT TTGTTTAACT 1700
AAACAGTGCT TTTTGCCATG CTTCTTGTTA ACTGCATAAA GAGGTAAGTG 1750
10 TCACTTG TCA GATTAGGACT TGTTTTGTTA TTTGCAACAA ACTGGAAAAC 1800
ATTATTTTGT TTTTACTAAA ACATTGTGTA ACATTGCATT GGAGAAGGGA 1850
TTGTCATGGC AATGTGATAT CACACAGTGG TGAAACAACA GTGAAGTGGG 1900
AAAGTTTATA TTGTTAGTTT TGAAAATTTT ATGAGTGTGA TTGCTGTATA 1950
CTTTTTTCTT TTTTGTATAA TGCTAAGTGA AATAAAGTTG GATTTGATGA 2000
15 CTTTACTCAA ATTCATTAGA AAGTAAATCA TAAAACTCTA TTACTTTATT 2050
ATTTTCTTCA ATTATTAATT AAGCATTGGT TATCTGGAAG TTTCTCCAG 2099

(2) INFORMATION FOR SEQUENCE ID NO: 26:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acids
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Ala Asp Pro Thr Gly His Ser Tyr

5

30

(2) INFORMATION FOR SEQUENCE ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
35 (B) TYPE: amino acids
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

40 Glu Val Val Pro Ile Ser His Leu Tyr

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(2) INFORMATION FOR SEQUENCE ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acids

10

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Glu Val Val Arg Ile Gly His Leu Tyr

15

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(2) INFORMATION FOR SEQUENCE ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acids

20

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

25

Glu Val Asp Pro Ile Gly His Leu Tyr

5

30

(2) INFORMATION FOR SEQUENCE ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acids

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Gly Val Asp Pro Ala Ser Asn Thr Tyr

5

40

57

- 5 (2) INFORMATION FOR SEQUENCE ID NO: 31:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acids
(D) TOPOLOGY: linear
10 (ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Glu Val Asp Pro Thr Ser Asn Thr Tyr
5

15

- (2) INFORMATION FOR SEQUENCE ID NO: 32:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
20 (B) TYPE: amino acids
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

25 Glu Ala Asp Pro Thr Ser Asn Thr Tyr
5

- (2) INFORMATION FOR SEQUENCE ID NO: 33:
30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acids
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Glu Ala Asp Pro Thr Ser Asn Thr Tyr
5

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- 5 (2) INFORMATION FOR SEQUENCE ID NO: 34:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acids
(D) TOPOLOGY: linear
10 (ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Glu Val Asp Pro Ile Gly His Val Tyr

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15

- (2) INFORMATION FOR SEQ ID NO: 35:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acid residues
20 (B) TYPE: amino acid
(D) TOPOLOGY: single
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Tyr Met Asn Gly Thr Met Ser Gln Val

5

25

- (2) INFORMATION FOR SEQ ID NO: 36:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acid residues
30 (B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

35

Met Leu Leu Ala Val Leu Tyr Cys Leu Leu

5

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- 5 (2) INFORMATION FOR SEQ ID NO: 37:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Met Leu Leu Ala Val Leu Tyr Cys Leu

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- 15
(2) INFORMATION FOR SEQ ID NO: 38:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acid residues
20 (B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Leu Leu Ala Val Leu Tyr Cys Leu Leu

5

- 25
(2) INFORMATION FOR SEQ ID NO: 39:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Ser Glu Ile Trp Arg Asp Ile Asp Phe Ala His Glu Ala

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- 5 (2) INFORMATION FOR SEQ ID NO: 40:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Ser Glu Ile Trp Arg Asp Ile Asp Phe Ala
5 10

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- (2) INFORMATION FOR SEQ ID NO: 41:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acid residues
20 (B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Ser Glu Ile Trp Arg Asp Ile Asp Phe
25 5

- (2) INFORMATION FOR SEQ ID NO: 42:
(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 16 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

35

Glu His Ser Ala Tyr Gly Glu Pro Arg Lys Leu Leu Thr Gln Asp Leu
5 10 15

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- 5 (2) INFORMATION FOR SEQ ID NO: 43:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Glu His Ser Ala Tyr Gly Glu Pro Arg Lys Leu Leu
5 10

- 15
(2) INFORMATION FOR SEQ ID NO: 44:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acid residues
20 (B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Ser Ala Tyr Gly Glu Pro Arg Lys Leu
25 5

- (2) INFORMATION FOR SEQ ID NO: 45:
(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 1032 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

35

CGCCAATTTA GGGTCTCCGG TATCTCCCGC TGAGCTGCTC TGTTCCCGGC TTAGAGGACC 60
AGGAGAAGGG GGAGCTGGAG GCTGGAGCCT GTAACACCGT GGCTCGTCTC ACTCTGGATG 120
GTGGTGGCAA CAGAGATGGC AGCGCAGCTG GAGTGTTAGG AGGGCGGCCT GAGCGGTAGG 180
40 AGTGGGGCTG GAGCAGTAAG ATGGCGGCCA GAGCGGTTTT TCTGGCATTG TCTGCCCAGC 240
TGCTCCAAGC CAGGCTGATG AAGGAGGAGT CCCCTGTGGT GAGCTGGAGG TTGGAGCCTG 300

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5 AAGACGGCAC AGCTCTGTGC TTCATCTTCT GAGGTTGTGG CAGCCACGGT GATGGAGACG 360
 GCAGCTCAAC AGGAGCAATA GGAGGAGATG GAGTTTCACT GTGTCAGCCA GGATGGTCTC 420
 GATCTCCTGA CCTCGTGATC CGCCCGCCTT GGCCTTCCAA AGTGCCGAGA TTACAGCGAT 480
 GTGCATTTTG TAAGCACTTT GGAGCCACTA TCAAATGCTG TGAAGAGAAA TGTACCCAGA 540
 TGTATCATTA TCCTTGTGCT GCAGGAGCCG GCTCCTTTCA GGATTTCACT CACATCTTCC 600
 10 TGCTTTGTCC AGAACACATT GACCAAGCTC CTGAAAGATG TAAGTTTACT ACGCATAGAC 660
 TTTTAACTT CAACCAATGT ATTTACTGAA AATAACAAAT GTTGTAAT CCCTGAGTGT 720
 TATTCTACTT GTATTAAGG GTAATAATAC ATAATCATTA AAATCTGAGG GATCATTGCC 780
 AGAGATTGTT GGGGAGGGAA ATGTTATCAA CGGTTTCATT GAAATTAAAT GTTATCAACG 840
 GTTTCATTGA AATTAAATCC AAAAAGTTAT TTCCTCAGAA AAATCAAATA AAGTTTGCAT 900
 15 GTTTTTTATT CTAAAACAT TTTAAAACC ACTGTAGAAT GATGTAAATA GGGACTGTGC 960
 AGTATTTCTG ACATATACTA TAAAATTATT AAAAAGTCAA TCAGTATTCA ACATCTTTTA 1020
 CACTAAAAAG CC 1032

(2) INFORMATION FOR SEQ ID NO: 46:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acid residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

25

Met Ala Ala Arg Ala Val Phe Leu Ala Leu Ser Ala Gln Leu Leu Gln
 5 10 15
 Ala Arg Leu Met Lys Glu
 20

30

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acid residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

35

Met Ala Ala Arg Ala Val Phe Leu Ala Leu Ser Ala Gln Leu Leu Gln
 5 10 15

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- 5 (2) INFORMATION FOR SEQ ID NO: 48:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acid residues
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Ala Ala Arg Ala Val Phe Leu Ala Leu
 5

- 15 (2) INFORMATION FOR SEQ ID NO: 49:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

25	ATG CGA AGA GAA GAT GCT CAC TTC ATC TAT GGT TAC CCC AAG AAG GGG	48
	Met Pro Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro Lys Lys Gly	
	5 10 15	
30	GAC GGC CAC TCT TAC ACC ACG GCT GAA GAG GCC GCT GGG ATC GGC ATC	96
	His Gly His Ser Tyr Thr Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile	
	20 25 30	
35	CTG ACA GTG ATC CTG GGA GTC TTA CTG CTC ATC GGC TGT TGG TAT TGT	144
	Leu Thr Val Ile Leu Gly Val Leu Leu leu Ile Gly Cys Trp Tyr Cys	
	35 40 45	
40	AGA AGA CGA AAT GGA TAC AGA GCC TTG ATG GAT AAA AGT CTT CAT GTT	192
	Arg Arg Arg Asn Gly Tyr Arg Ala Leu Met Asp Lys Ser Leu His Val	
	50 55 60	
	GGC ACT CAA TGT GCC TTA ACA AGA AGA TGC CCA CAA GAA GGG TTT GAT	240

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5 Gly Thr Gln Cys Ala Leu Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp
 65 70 75 80
 CAT CGG GAC AGC AAA GTG TCT CTT CAA GAG AAA AAC TGT GAA CCT GTG 288
 His Arg Asp Ser Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val
 10 85 90 95
 GTT CCC AAT GCT CCA CCT GCT TAT GAG AAA CTC TCT GCA GAA CAG TCA 336
 Val Pro Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser
 100 105 110
 15 CCA CCA CCT TAT TCA CCT 354
 Pro Pro Pro Tyr Ser Pro
 115
 20 (2) INFORMATION FOR SEQ ID NO: 50:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 676 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:
 30 TCTTCATACA CGCGGCCAGC CAGCAGACAG AGGACTCTCA TTAAGGAAGG TGTCTGTGTC 60
 CCTGACCCTA CAAGATGCCA AGAGAAGATG CTCACCTTCAT CTATGGTTAC CCCAAGAAGG 120
 GGCACGGCCA CTCTTACACC ACGGCTGAAC AGGCCGCTGG GATCGGCATC CTGACAGTGA 180
 TCCTGGGAGT CTTACTGCTC ATCGGCTGTT GGTATTGTAG AAGACGAAAT GGATACAGAG 240
 CCTTGATGGA TAAAAGTCTT CATGTTGGCA CTCAATGTGC CTTAACAAGA AGATGCCCAC 300
 AAGAAGGGTT TGATCATCGG GACAGCAAAG TGTCTCTTCA AGAGAAAAAC TGTGAACCTG 360
 35 TGGTTCCCAA TGCTGCAGGT GCTTATGAGA AACTCTCTGC AGAACAGTCA GGACCACCTT 420
 ATTCACCTTA AGAGCCAGCG AGACACCTGA GACATGGCTG AAATTATTTT TCTCACACTT 480
 TTGCTTGAAT TTAATACAGA CATCTAATGT TCTCCTTTGG AATCCTGTAG GAAAAATGCA 540
 AGCCATCTCT AATAATAAGT CAGTGTTAAA ATTTTAGTAG GTCCGCTAGC AGTACTAATC 600
 ATGTGAGGAA ATGATGAGAA ATATTAAATT GGGAAACTC CATCAATAAA TGTTGCAAAT 660
 40 GCATAGTAAA AAAAAA

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(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13585 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) FEATURE:

15

(D) OTHER INFORMATION: at positions 9421-9456, the "Ns"
refer to an unsequenced portion of
from 4.7 to 5.3 kilobases

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

20

CCGTCAGAAA TCTAAACCCG TGACTATCAT GGGACTCAAA ACCAGCCCAA AAAATAAGTC 60
AAAACGATTA AGAGCCAGAG AAGCAGTCTT CATAACGCG GCCAGCCAGC AGACAGAGGA 120
CTCTCATTAA GGAAGGTAAG AGCGTTGCCT TCTCGCCATA ATCATAGTCC TCTTCTCCA 180
GAATAGGATT TGGGAAATTC TGGCTAAGTC CTCTGCCTAC CCTCATTGCC CCGCTGATGT 240
GTGACATCAA CAGAATTTCT CCGCAACGTT TGTCAGTCTC CAACCTCAGA GGGCTCACAA 300
25 AGCCTCCTCC TGAATCCTCT CTCAGTCCTC CAACACTACC AAGAAGAAAA GCAATTATTC 360
AGGATGGCAT CTTGCTGGGG AGAAGCAGCC TCCCTGAGGT AGATGTGTTT TCCTGTCACT 420
TAAAGAACCA CTTCTCCTGG TCTGAGTAGT AAGAGGCGCA TTTGCTGTTG CTGCACCATT 480
TGCCAAGGCT CTGAGTTTGA GGTATGGGAT GTATTAAAC AATTTAATGA AGAATTAAGA 540
TTCCATTCTG TCATTTTGAA CACAGGGTTC AGTCCTATAT TATTCATTG AGAGGACTGG 600
30 TGAGTTTGAC TTTCAATTTCT TTTTACAAC TGGGAAGGGC AAATTACACA TAAATGTCC 660
CAGTGGAAAG GGGTCATGTG TCGAAATCCC CACTCTTCTG TCTCACCTCT CCCTGTTGTT 720
TTAAACTGGG GCTCATTAAAT ATAATTCTAT GGGGATCACA CCTTTGAAAT TCATGAGGAC 780
AGTAAGAGAG CAGAAAAATA CACAATAATA AGGAAAGGAG CTTCCATTAT TGGTTTTTAA 840
TGAGCGTACT TGAATTACGG CCACTGCaGT TTATGGATAT TTTTGTGTTG TCATTTGTAT 900
35 GTGTTATAGT TAGAAAAAAA AAGAATCCTA GCCAAGGGAC TTGAACCAGA GAGAAGCAGA 960
AATTGACTTA AGTAGGAAGG GAAACACATT ATTAGATAAA GTCAGGTCCT GGGCTTCCTC 1020
GGCTTGTTTT GGGTGGAGTG CCTGGGGACA GGCTGAAGCC CCTGTGTGGG GTGGTTTCCT 1080
TTGCTGAAAA GCTGGGCTGG AAGATGTTGT GCTCAGTGCT CAACCTCATG CACCCTCGCG 1140
AGGCACAGGC AACGGGTGCT CTGGGAAACA CAGTTATGT ATCATAGCCT CTGTTTGTCT 1200
40 GTGGGATTGA TATCCAATAA TAACTTTGGA GAAAAATAAC TCCTCTTATT TTGTTAGCCA 1260
CAGCCCTGGG CCAGGGAAGG TGGAGAATCA GTGAAATGC ATTTTGTGTTG TTTCTCTAGA 1320

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5	AGTTTATGGT GCAGAGTCAA ATTGAAGGCA AATGAGGAAT ATTTTTCAT TAAATAATAA	1380
	CTCAACTTGC AAGTCTTTTT TGCTTTTGT TGTAGTTTCT TCTTTGAACT TAATTTTCAG	1440
	TTAGTAGGAG GGGTTAGAAA CCTGAGCTAT TGCTAAAGCC CTTGATATGA ATGAAAGAAG	1500
	CAGGTGCAAA TCCCCTCACA GAGAGAAACC AAAGGGTCCT GGCTATGGAT ATTGGTCACC	1560
	TAGTCAGGAT GCTGTTGTGG GTCTTTATGA GATGATGAAT AGGGTGGCTT TGGATGCATT	1620
10	AATGATATTT ACATGCTCCT TCTGTTAGTG TCCTGTGCCC TGACCCTACA AGATGCCAAG	1680
	AGAAGATGCT CACTTCATCT ATGGTTACCC CAAGAAGGGG CACGGCCACT CTTACACCAC	1740
	GGCTGAAGAG TAAGTTCAAA ACCAGACCCA GCAGGGCTTC CAGTTTGCCG TTTGCTGACA	1800
	CAGCCTGCTG ACTTCCACCA GTACATGCCT GCTCGTAAAT CTCCCTAGTG TTTATCTCCC	1860
	CAGACAGTAA CATCCCTGGC AACAAGGGGA GGAGATTCTG TGCTTCTATA AGGGGCTCAG	1920
15	TCAAGCTTCT CTGAGGCCAA ACAGGCAGGA AGATGGGAAT GGTATAAGGT TGGATCTTGC	1980
	CATTTTTGGG TGCACTTTTG ACTATTGGGT CTTATCTGTA GGTTCCCAAG TGGAAAAACA	2040
	TCTGTTCAAG ATCACAATGC CTCTCTCCTC AATCCTTGTT CTGTCTCCTC CACTCAAATT	2100
	CCTGAAGGTG GTTTGCAGAC AGAATAAAAG TGAGTTGCCA AGGAGCCAGT AAGGATGACG	2160
	GGCAGGTGTG TGTGACTCAG CCCACAGCCA GACTCGAGAG GAAGATGGAG GTCACAGCCT	2220
20	TTGCAGTATA ACTTTATCCT AAGGAAAGAC ATTGGGTTTT ATGAGTGAAT TAAAAATAAG	2280
	TATTTATATG ATTAAGCATT TCTAAATGCT AAGCATTGTA TACTGGCGTG AGACACTGTT	2340
	TTTATCTTTG AAAAACTCA CAACTTAGTG GGAGAGTTAG GCATGAGATT AATTTAGCA	2400
	AATGTAAGTG CGGTAATGAA AACCCAGAGG CTGCAGGGAC ATACTCTGTA TGTGCTGGGA	2460
	GTGGGAAAGG GACATACTCT GTACGTGCTG GGTGGCAGGG GCAGGGGAGG CCCCACCCTC	2520
25	TGCGTGGGAC TGTAACAGGA CAACACCCTC TTATGTGGTC TGTCCAGAAC TCCCTGTGAA	2580
	CCTGCTCTTT CTTTGGAAG AGCTGTTGAA CAATCTTGT TAACAGTCAA CCGCAGGACC	2640
	AGCAAGATGT AAAGCCCAAC AAAGGCACTG AGGAAGAGTT CAGGAAGACA GCATTTCTCT	2700
	AGAAGACCCT GGTATAGGAT CCTCTAATAT CCCTGGCCAA TTGGAGATGA GGGCGGCGGT	2760
	ATCCTCTCAG AAAATGTCCT GACAGCAAAA ACATACTCTT TGAGGGAGGG GAGCCCATTG	2820
30	CCCGTGCTAT TAGTTAGGGT ATCGTTTCAG CTTGTGTATA ATCACTCAAC AGACTCTTTA	2880
	AAATATACTT TTATGTCTCG TGTA AAAAATT CAAGAGTAAA GAGTTCAAGG CCTGTTTCGT	2940
	TTCTTCTTGC TGTTTACTCC CTTGGGATCG TCACTTTTGT CCCCATGGCT GAAGATGTTG	3000
	TGCCATCACC TCCACATCTT GCCAACAGAA AGCAGGAGGT GAAGGAGAGG CTAGGACCAT	3060
	TCCTTTCAAG GGGCACACGT CACTTCTGCT TATTGCTCCA CCCCCGCCCC CCGCCCCGTG	3120
35	GCACCCACCC TGGTGGTATC ATTCTTGCTG TGTGTAAAT GAAGAAAGGT TTAGAGAAAT	3180
	TAGGAAATGT GTGGCCAGAC ATGGTGGCGC TGGGATTAA ATCCAGGTCT GTTTGCCTCC	3240
	AGAGTCCATG CTCTTAAGTG TTATGCTGCA GGCCAGCAGA GGCAATATT TGCACAATCC	3300
	CATCCGACGA GAGGCTAGGG CAGAGGTCAG TATCTCTCAG TGTGAAGCTG GAGGCTGATG	3360
	CTAGTCAGCT CAGTAGGCCG AAAGTGGAGT TGTCCTTTGC CATGTAGGGC CATCATGCCC	3420
40	AGCTGGGGAA CCTCATAGCC AGGTGTACCC ACAACCTGAA CAAGGTAAT TTCAGGGTCT	3480
	AGTCAGGAAG AAACCAACTA GATGGTTCAA CATAGAGACT TTAATATAAG AAGCTGGTTA	3540

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5	AACAGGCATG GGA CTGAGAC TGAGGAGGCA AAGAAGGCAT CGGGGCAACC AAGGCTGTAC	3600
	CCACAGAATG CTGCTTCTAC CCCC GTGTCT GGGGTAACAA ACGGAAGGGT GAGGCCATCA	3660
	GGACCTAGAG TTGGGAGGAG GGACGCCACA GAAATGGGAC CCAGATCTCT AAGGAGAGAT	3720
	TTTTGTTTGG CTGGTTCTGG TGTCTCAAGA GCTTAGAAGT GAGGGGCATG AATCAAATAC	3780
	TCAGGCCTCT GAGGTCAGCC AGTGCTCTGC TGGGGAGGGG CATAATGAAG CTGGCTCTGA	3840
10	CAATGCCGGA AAACGAGCTG GTGCTTGCCA TATACAGACA ATGTGAGCAT TGCTGGGGTG	3900
	ATCCTGACAG GAGCCAGAAG CACACTGGAA GGAGCTGCTC CTTCTTGATG CCCCAGGTTT	3960
	GTAGGCACCC TCTAGAGTAC TCTAATGGGA GCCAGTGGGC AAAGGAGAAG TGGCATTTGC	4020
	AGAGTCCAGT CCCAGCATCA CAGAGCAGAG CATAGAAAGG TAGGTTTGA GAAGAGGGAC	4080
	AATGGCTTAA TAAAGGGCAA AGGGGGTTAT GACCACTATC ATGTGAAGGA ACCCCTTGAC	4140
15	TGAAGGCACA AGCTTTCTGT GTCTTGCAAC CTGAATGACG TGCATAAGCA GGGTCAGGTG	4200
	GGTTATCTGA CATTTTCCTT GAGAACAAGA GGGAGCCTCT GGATTCCAGC ACAAAGAAA	4260
	AATACCCACT CAACCCGTAT GCGTGGGAGC TATCCTTTAA AGAGAAAGTA ATTCTTTTG	4320
	ACATTTTGCT GTCTGTAGAA GGGTCAGATG GCCAAAGCTT CCAGCACAAT GAAACACTTA	4380
	ACTTCAGTCT GTGAGTGTAG GAACCCCTGA ATACATGGAA CATCATCATC TTGTGCAGGT	4440
20	ACTGAAGGAG ATCGGTCCAG AAAATAAGTA ACTGCACATG GCCACCAATG TCAAAGTCA	4500
	TTCTCTCAT GAAAAGTCCC TGCCCCATT GCTGTTTGT TAAATAGGTG GGATGGAGGT	4560
	AGGGGAATGG GGCCATCTTC TTTTTTTTTT TTTAATTTT TTGCATAAAA TCCAGATCCT	4620
	GCACAATGGG GCAATCTTCA TAAAACAAT GCATCCCTAA GATCTGAGAA TATTTATCCT	4680
	TCTACAATT GTGCCAGCAG GTGGAATGAA GAAGAATGAT GCAAAATAAG TTCCCACATC	4740
25	CAGCCAAGAA GGA CTACATA CCTGCTTGG GTATTATGTA TCCCTTTGAA ACCTCAGTGG	4800
	AGAGCAGTTC TCACAGTTGG GTGGACACAA GTCATCCATG GAACTTGTTA AAATGCAGAT	4860
	TTCTAGGTGC TGCCACCTAA GAGGCTGATT GGGTAGGCCA GGGGTGGAGT CCTATGATCT	4920
	GCACCTTAAC GTGCATCTCA GGTGATTCTG CTGCAGGTGG TATTTGGAAG ACACTCTGAG	4980
	GCGCCCTGCC AAGCTGGGCA GTGGGTCTT CCAATGTGTC AGGCATACCC TGGTGCTTTT	5040
30	CGCTCTCAGT CACTTGGGCA TGTGTGAGT ACCACGTGAC CATGCATAAA GTGCTGTAAC	5100
	AGAGCTCTGT CTGTGTCAAG ATATTCAAGT GGACGCCACA GGGTAAAATG AGAGCACAGG	5160
	CATGTTGGGA GTTGAATCAG CTGCCTTCAG TCACGAGAAC AACTGAACA CTCCTTGTA	5220
	CAGCTTCAGT TCAGGAAAGA GTGACTCTGC AGGAAAAGCA CTGGCCTGGG AGACCTGGAT	5280
	CTGGCCCAA TTCTGGTGCT CACTTGCTTG GTCTCCCGTT CCAGTTGCTG TGAATGTTGG	5340
35	TTCTGCCACT TGCTGGTTGT GCAGCCCTGG GCACTTGACC AGCATAATGT CAGCTGTAAA	5400
	ATGAACATCA TTCCTAACTC CGAGGACTGT GGTTAGGATG AAATAAAAGC ATATATGTGG	5460
	GGGTGCCTAG CCCAGTGCCT GGCACAAATT GGTGCTCAAT GAATGGTAGT CACTATGGTT	5520
	ATGGTAATGT TGATGAATCT TCATAGGTCT CAGCTTCCTG ATCTATAAAG CGGGTGGACT	5580
	GACCTACATA AGTCAGAGTT TCCATCTAGC ACTGTCATCC CATGGTTTCG TCTATCCTGT	5640
40	TTGGAGACGG ACAGGATAAG CTTGATGTCT CCTCAGCCTT GAGACAGAAG TTGTCCAGTA	5700

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5	GATGGTACTG AGCAAAAGTC TCTCCAGCAG AAGCCTTAGT TAAACCTTGC TTCTCCTGTA	5760
	GCTGCTCAGT CTCTTGTAAG TCACTCAGCT CTGCAGAAAC TTTCTTAGCG AGTTGACAAC	5820
	CACAGATAAC AGAGTCAGTT CTGTCGATTT TGATCATGCT GTGATCAGGC AGATGTTAGC	5880
	TAATTGATGA TGCTTGCCCG GAGTGAACAG CTCCAGGCCG TGTTCCTCAGG GTCTTTGTGG	5940
	TAACTTTGTG GTAAGTGTAA TGCTTCCCAG GGGTCACTGA ACACAGGGCC CAAGAGGCTG	6000
10	GTGTAGACCC CCAGATTGGC ACCCTGCTGC TTAGACAAGA TCCTTCTCAA TAAGTAATGC	6060
	CATAGCTTTG CTGTAGGTTG AGCCAGACA CTTCTCCCTA GGGCTGCAAG GAGCAAAGCG	6120
	GGGAGTTTAG GGAAGGGAGG GCACGAACAT AATTGAGACG GATTCAGGTT CAAATCCAGC	6180
	CTCTGTTTTG TGCTAGCTCT GTATGATCAC CAGCGAGTCA TGTATCCTCT GCCTTTTATT	6240
	TCCTCTTCTG TGAAAATAGG GGATGATAAA TTGTGTCTAC CCTCCAGTGT TGATGTGAGA	6300
15	ATTGAATAAG CTAATGAATG TTTAGCACAG CACCTGGCTT TTAGTAGATG AGTCAGTGTT	6360
	AATTTCTATT TTCTCTTTGT GGGCTGAGTT GGAGAAAATG TTTTAAACA GCCTGATGAG	6420
	AAGAAAAGAT AATTTAGCCC CAATAAATAC ATTGTCCACA TAAAGACAGT TACTATGGCA	6480
	CTTCTCATAC CTGGAAGTTG GGTGCCTGGG CCATGCAATT AGCAGAGTTC CTGTGGGCAC	6540
	ACACTTGAGA GGCTCCTAAA GACCTGGGTT AGATCCAGGT GCTGGAGGCC TGGTGGGGTG	6600
20	CCAGTGTGGG AGGTGGGAAA CTAAGTGGAC ACTGGGAGAT GCTGCTCTGG GTCGTCAAAG	6660
	TCCATATGAA GAGGAAGACT GATTTATGCT TCATCATAAT GTAGAACAAT GTTTCAATGA	6720
	CAAAGTGGAT TTGTCTATCT CTTGGGCCAG GCCGCTGGGA TCGGCATCCT GACAGTGATC	6780
	CTGGGAGTCT TACTGCTCAT CGGCTGTTGG TATTGTAGAA GACGAAATGG ATACAGAGCC	6840
	TTGATGGTTG GTAAAGTTCC CACTGCTGAA ATCCCTCCAA GTCCAGGGCC CTCTTTCCAG	6900
25	TTCTTTCTC TGAATCTCTG GAGAGTCAGA TAATTGCCTC ATTATAACCT TCAGCTCTGA	6960
	TTCCGGCTTC TGATGCCTCT TTTGCTACAT TGTACTTTGG CAACTCTACC TTTGCCTCTG	7020
	CTCAGGCATG AACCTCAACC AGGAACTTGC CCTGTGTCTT AGTCTGTGAT TATAACATAA	7080
	TACGAGAGAC TGTAATTTAT AAATAAATGA AATTCATTTG GTTTACAGTT GGGAGGCTGG	7140
	GAACTCCAAG ATCTAGGGGC CACACCTGGT GAGGACTTCT TGCTGTGTCA TATCATAGTG	7200
30	GAAGGCATCA CATGGGCAAG GGAGTGAGAG AGCAAGAGGG AGCTGAACTC ATTTTTTTTT	7260
	TTTCTTGAAA CAGGAAATCC TGGGATGGAG CGCAGTGGTG ATCATGAGTC ACTGTAGCCT	7320
	TGACCTCCTG GGCTCAAGCC ATCCTCCTGT CTCAGCCTCC AGAGTAGCTG GGACCACAGG	7380
	CACGTGCCAC CACACCGGCT AATTAAAAA AACTTTTTT TTGTAGAGAC GAGGTCCCAC	7440
	TATGTTGCCC TAGGCTGGTC TCAAACCTCT GGGCTAAAGT GATCCTGCCT CGGCCTCCCA	7500
35	AAGTGTTGGG ACTACAAGTG TGAAACACTC CACATATGGC CCAAACCTCAC TTTTATAACC	7560
	AACCTACTTT TGCAATAACA AACACACTCC TGCAATAACA CAATTAATCC ATTCGATGAG	7620
	GACAGAGCCC TTGTAACCTA ATCGACCTCT TAAAGTCCT GCCTGTTACC ATTGTTGCAT	7680
	TGGGGATTAG GTTTCCAATA CACGAATTTT GGGGGACACA TTCAAACCTAT AGCACCTGTC	7740
	TCTTTGGTTC TACTCATAGC AGACTTGGGT ACCTGGATGT TGTGTGTAGC TAAGCACTGA	7800
40	CGGTTTATAG GGCACAGGGG AAGGGGTTTG AGGTTCCCTT ATAGCAAACA GGAGTATATT	7860
	AGACACCTCA GGTTTTACCA CTTCTGGGAA TTCTTGCTGG TTCTGTTACT CCACTTTGTG	7920

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ACCTGCTCTT CCTACTTTTC TTCTTCACCC CTTTCCTCAC TGGTTACCTG TGAATTCCAA 7980
GTTCTTCTGA CTCTACACTA AGCATCCCAG GATATCATCA GTGCGATGAG GAAACCATCC 8040
TTCTGTCATC AGCACAAAGG GTCACTTGTG TGT TTTTAA CAGGCTGCAT CCTTCTTAGA 8100
TGGCCAAAGG TTTTAATAGT ATTTTTTCT TCTTTACCCA AATATGCAGG AAGCTAACAC 8160
AATTACACAA TCCAATCTTC TGGTACCAGT ATCCTCCATG AATGGGAAAC ATCAACTGAG 8220
TTTATAAGCT ATAAAAATTA CAGGTTTCAG CAATCTTGCT TAAAGCCAGG TAGCACTTCA 8280
GCACTTCAGC ACCCGAAGCA TTCTCCATAG ATCTCGCTGT CTCTCTTCT TGTATTACA 8340
GATCTGAAAG CTTTTCAGGT TGATGCATAA TGGAAAAAAA GTATCTTCC AAAAGATGTT 8400
GGAAAGTCCC ATTCTCATT AGCAAGCACT TCATTAGAG GAAAAGGTCC TGTGAAAGAG 8460
AGGAGGGTTG GTGTGGGGTG GGGATTGAAG CTTGGCAAGC TGATAAGGAG AAGGTGAGAG 8520
ATACAACTCT GGATTCTTTC CCTCTTGCC AAGAACTTG GGCAGTCTCA TGTCTCATGT 8580
CTCTGTTCC CCAATGTCTT TCCAGAGCAT AAATACAAAT ACAAACCATC AAAGGCAAGT 8640
CAAGTCTGGG GGCTGACACA CCCACCGAGC ATAGCCCTCT AGTGTGCTGA CATCTAGTGG 8700
GAAGGAGGAG GAGTTGATGA ATCTGAACAA GACTCCAATA TTGGAGGAAA TACTTGAGGA 8760
AAGCCTTGGG TTAGAAAGTT AGGGATAGAA TTCCTGCTCA TACGGCTGTC CACAACAGGT 8820
TAGTAGGGGA GGACTTTAAT CTCTGCCATA GAACTCCATT TGTAAGTCTA GCATGGGGTT 8880
ATGACATTGC CTTGTAATTG GCTATTTACT TTTTGCCCTC TCGACCCCTC CGCTTTCCCC 8940
TATGTATGAA CCACAACAGA GAATATTTCT AACTCATCTT CATATCTCCA GTGCCTAGCA 9000
CAGTGCCTGG TACATGGTAG TCACTCAATT GTGTTGCATT AGGACTTGGT CCCATTGTCT 9060
GCCATTGAGT TGCTTGAGAG CTAGAATTCA ACTTCTCCAA GATTCACTAG CTCTATTTTA 9120
CAGGAGGAG TGTGGAAT CTGTGATGTA ACACAATGTA TATCCATTTT TATTTAATAC 9180
ATATTTCTT CTATATTTTG ATTTTATTAT ATATTTGTAT ATCAAAAACA AAATGTTTAG 9240
TCTTTCAAGA AGTAAAGCTA TACAACTCA ATATGTTGGT ACTCATTTCC TAACTATAAT 9300
TATTAGTTTG ATCCTATTGA ACACAAATGC AGTAATTTT CTTTCTGCT TCAATGCTCT 9360
CATCTTAAAT TCATTTAATT GAAAAATAAC AGAGAGTCTT AATGTCATGT GTCAGACAC 9420
TNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNGAGT GCAGTGGTAT GATCTGGGCT 9480
CACTGCAAGC TCTGCCTCCT GGGTTCATGC CATTCTCCTG ACTCAGCCTC CCAAGTAGCT 9540
GGGACTACAG GTGCCCGCTA CCATGCCTGG CTAATTTTTT GTATTTATAG TAGAGATGTC 9600
ATTTCACTGT GTTAGCCAGG ATGGTCTCAA TCTCCTGACC TCGTGATCCA CACGCCTTGA 9660
CCTCCCAAAG TGCTGCGATT ACAGGTGTGA GCCACCGTGC CCGGCCTTAT ACTTCTTTT 9720
TACTTTTTTT CAGTGGTTTC CCTAGAGTTT GCAACATACA TTTACAATA ATTCAAATCC 9780
ACTTTCAAAT AACACTATAC CATTTCATAG GCATTATGAG TATCTTAAAA TAATCCTAAT 9840
TCCTTCCTCC TGTAACATAA AAACAAAATC CTAAATCCTC CAAACAACCTG AATGGACCCC 9900
CTCTTCACCA AGGGGACCCC AGGGAAACCT GAAAAACTGA GTGTTGGCCA TGACGGGAAG 9960
GGAGGTGAGA GATGCTCATT ATACTCCCTC CCTTTTAGAG TTTTAGGTAC AACTGACCAG 10020

5	CATTAATTTT AAAATAGAGA TTACAGGACT GACAGAATGA ACTCTTTGTG GCAATATCAA	10080
	ATTAGGAACA AGACAATGCA AGGAAAGGGT TAAATCATGC CCTTCAAACC ATAAAAAAT	10140
	TTTTTTTAA TTAACCCCAT ATAATGTGGT ATACTTTCCA AACTGACTCT GGTATAGCAT	10200
	CACATGACAG ATTGCAGACT CCCTTACCTT AAGCATTCTT TTATACTGAC TTCAAGTCTT	10260
	AAGACAGAGC TGAACCTTTT CAACCAGCTG CTAACATAAG AATACCTAAA ACCCACCTGT	10320
10	GACTTGTAAG TCTCTGCTTT GCCATGTCCT GCCTTTTCAG GCTGACCCAA TGTATACCTT	10380
	CCGTGTATTG ATTTATGATT TTTACCTACA ATTCTGTCT TCCTGAAACA TATAAAACCA	10440
	AATCATAACC CAACCACCTC AGGCACACTT TCTCAGGACC TCTTGAGACT ATTCTCCCGG	10500
	CCATGGTCAT TCATATCGGC ACAGAATGAA ACCTCTTTAA AATATTTTGC AGTTTTTTTC	10560
	TTTCTGTAA CATTCCTTTC CTTGTATCA TTGCTGTTAT TAATTTCAAG TATATATAAG	10620
15	CATACCTAAT TAAATACATT GTTGCTATTA TTCATTTTGG AACAACTAT TATCTGTAA	10680
	ATCAACTAAG AATAAGACAA ATATGTTGGG TGCAGTGGTG CATGCCTATA GTCTCAGCTA	10740
	CTCAGAGGCT GAGGCAGGAG GATTGCTTGA GCTCAGGAGT TTAAGACCAG CCTAGGCAAC	10800
	TTAGCAAGAT CATGTCTCTT AAAAAAAAAA AAAGAAAGAA AGAAAAACAA AGTTTLAGGA	10860
	GGCTGAGGCA GGAGTATCAC TTGAACCCAG GACGCAGAGG TTGCAGTGAG CCGAGATCGT	10920
20	GCCATTATAC TCCAGCCTGG GCAACAGAGT GAGACTCTGT CTCAAAAAAA AAAAAGAAAA	10980
	GAAAAGAAAA GAAAAAAAAA GTTTTTATTT TACCTTCACT TATTCCTTCT TGGATGTTCT	11040
	TCCTTTATGT AGGTACAAGG TTCTGACCTA TGTTATTTTC TTTTCTCTA AAGAACTTCA	11100
	AAAGTTTCCT GCAAGGCAGG TCTACTGGCA ATGAATTCCC TCAATTTTGG CTTGACAAAG	11160
	TCTTTATTTT TGCTTCACTA TTGATGGATA ATTTCAACAAG AGTGTTCTT TTGTAGATTC	11220
25	ACTCTTCTTA TCCTTCCCTT CAGAAATATT CTTTGACCAA CTATTGGGTC CCAGGTACTG	11280
	CACTAGAGCT TACTTCTAG TTAATTCCCA CAGCAATTCT GAGAGGTAGG TAGGTATTAT	11340
	ATTCCTAGAT GCAAACCTCAG AATTCAGAAG GTAAAGTGAT GAGACTGAAG GCACACAGCA	11400
	AGTAAGTGGC AGAACCTAGA TTAAACTCA TTCTTAAAC TTTGGCTTCC TTCTCTTTTC	11460
	TTTAATGGAT TCAGTTACTT CTCTCACCC ACTCACCTT ATCAATTTAC ATTTAGATA	11520
30	AAAGTCTTCA TGTTGGCANC TCAATGTGCC TTAACAAGAA GATGCCCAACA AGAAGGGTTT	11580
	GATCATCGGG ACAGCAAAGT GTCTCTTCAA GAGAAAACT GTGAACCTGT GGTAGGTAA	11640
	GATCCTTCAT AAGGGTATTT TCATGAATGG CTGTTTTTAA CTCAAGTGAA TACAATTATT	11700
	TCCATTTAAA AAGCAAGGAC AATGTGAATG TACTCATTGC CACTGAACTA TATACACCTA	11760
	AAAATGGTTA AAATGGCAAC TTTTATGTGT ATTTTATGAG AATAAAAAAT AAATAATAAT	11820
35	AAAAACAAG GGAAGTACAG ATATTTTCTT AATTGTGTTG TCACATACCC AGTGTTTCCA	11880
	GGGTCAATAA TGAGAGCCCT ACATGTAAGA TTCAAAGGAA GAATTTAGTC CTGGATACAA	11940
	TATCTTTTAA TGTTTTTAGT TATATTGCC TTTTAAATGG ATGCAGATAT ATACAGAGGG	12000
	AAGGGATAAA GTACCTATTA TTTATTGTAT AGAGCTGTGC TGTCTGATGG CTTAGCCACT	12060
	AGTCACATGG TGCTATTGAA CACTTAAAC ACAGGAGTTT GAAATAAGCA TGTATTATAA	12120
40	TACATATCAT ATTTCAAAAA TATTAGTATG TAGAAAAGAA GATAAATGGT TCATTAATGA	12180
	TTTTTATATT GATTCACCTT GAAATAAATA TTCTGAAAAT ATTAGGTAA ACAAATATT	12240

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5 TTAAGATTAA TTTTACATGT TTCTTCTTTT AAATGTAGCT ACTAGAAATT TTAAAATTAC 12300
 ATATGGCTGG GCATGGTGGC TCACACCTGT AATCCCAGCA CTCGGGAGG CCGAGGTGGG 12360
 TGGATCACCT GATCTCAGGA GCTCGAGACC AGCCTGGCAA ACATGGTGAA ATCCTATCTT 12420
 TACTAAAAAT AAAAAATTA GCCAAGCGTG GTGGTGCATG CCTGTAATCC CAGCTACTTG 12480
 GGACGCTGAG GCAGGAGAAT CACTTGAACC CGGGAGGTGG AGGTTGCAGT GAGCCGAGAT 12540
 10 AGTGCCACTG CACTCCAGCC TGGGAGACAA GAGCAAAACT CCATCTCAAA AATAAATAAA 12600
 TAAAAATAAA TTACATAAGT GGCTTGTACC ATATTCTAT TGGACAGCAC TAGTACATAT 12660
 ACAACACAGC ATAATGGTTG AGAGCACTGA CTCTGGAGCC AAATTACTGT GTTTGATTCT 12720
 TAGCTCCACA ACTTACTAGT TGTGTGACCA TGGGCAAGCG AGTTAACCTC TCTGTGCCCC 12780
 AGTTTCCCAT TCTGTAACAT GAAAATAATA AAAACACTCC CCAGAATTGT TGTGAGCATT 12840
 15 AAATGAAGCC CTGACACATT TGTCTGGAT ACAATATCCT CTTGTTTTAT ATTTGGTAGT 12900
 ATCAATGTGC CTTTAGACAC AATTACAACG ATCTCTGTGG TAAAGATGCA ATGTATATGG 12960
 TGTCTATAAA TAGCATTCAA TGATTGCTTA GTTAGGGCTT GAGACTTTTA CTGTCATGGA 13020
 AAATCTAGGT ATAGCTAAGC TTTTGAGATT TTGGGAACTC CTTAACCTA TTTTCTCTA 13080
 CTCTGCCCC CAACAATCAG CCTATATACT TGTGAAATTT AACAATTACT TCACTGGGCA 13140
 20 GAAATTATAT GGGAACACTT AGAAATTTCA GTCCACAGGG AAAGTATAAA TATGTAACT 13200
 ATTTTAACTT AATCCCTTCC TAGAAACACA TACACTGTTG CCAAGCCCAT ATTCTCCCTT 13260
 TCTTGTTCTC ACAGTTCCCA ATGCTCCACC TGCTTATGAG AAATCTCTCTG CAGAACAGTC 13320
 ACCACCACCT TATTCACCTT AAGAGCCAGC GAGACACCTG AGACATGCTG AAATTATTTC 13380
 TCTCACACTT TTGCTTGAAT TTAATACAGA CATCTAATGT TCTCCTTTGG AATGGTGTAG 13440
 25 GAAAAATGCA AGCCATCTCT AATAATAAGT CAGTGTTAAA ATTTTAGTAG GTCCGCTAGC 13500
 AGTACTAATC ATGTGAGGAA ATGATGAGAA ATATTAAATT GGGAAAACTC CATCAATAAA 13560
 TGTGCAATG CATGATAAAA AAAAA 13585

(2) INFORMATION FOR SEQUENCE ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 648 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

35 AGCTGCCGTC CGGACTCTTT TTCCTCTACT GAGATTCATC TGTGTGAAAT ATGAGTTGGC 60
 GAGGAAGATC GACCTATCGG CCTAGACCAA GACGCTACGT AGAGCCTCCT GAAATGATTG 120
 GGCCTATGCG GCCCGAGCAG TTCAGTGATG AAGTGAACCC AGCAACACCT GAAGAAGGGG 180
 40 AACCAGCAAC TCAACGTCAG GATCCTGCAG CTGCTCAGGA GGGAGAGGAT GAGGGAGCAT 240
 CTGCAGGTCA AGGGCCGAAG CCTGAAGCTG ATAGCCAGGA ACAGGGTCAC CCACAGACTG 300

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5 CTGCAGGTCA AGGGCCGAAG CCTGAAGCTG ATAGCCAGGA ACAGGGTCAC CCACAGACTG 300
 GGTGTGAGTG TGAAGATGGT CCTGATGGGC AGGAGATGGA CCCGCCAAAT CCAGAGGAGG 360
 TGAAAACGCC TGAAGAAGAG ATGAGGTCTC ACTATGTTGC CCAGACTGGG ATTCTCTGGC 420
 TTTTAATGAA CAATTGCTTC TTAAATCTTT CCCACGGAA ACCTTGAGTG ACTGAAATAT 480
 CAAATGGCGA GAGACCGTTT AGTTCCTATC ATCTGTGGCA TGTGAAGGGC AATCACAGTG 540
 10 TTAAAAGAAG ACATGCTGAA ATGTTGCAGG CTGCTCCTAT GTTGGAAAAT TCTTCATTGA 600
 AGTTCTCCCA ATAAAGCTTT ACAGCCTTCT GCAAAGAAAA AAAAAAAA 648

(2) INFORMATION FOR SEQUENCE ID NO: 53:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acid residues
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Ala Leu Ser Arg Lys Val Ala Glu Leu

5

25

(2) INFORMATION FOR SEQUENCE ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acid residues
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Phe Leu Trp Gly Pro Arg Ala Leu Val

35

5

(2) INFORMATION FOR SEQUENCE ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acid residues
 - (B) TYPE: amino acid
- 40

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- 5 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

10 Thr Leu Val Glu Val Thr Leu Gly Glu Val
5 10

(2) INFORMATION FOR SEQUENCE ID NO: 56:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

20 Ala Leu Ser Arg Lys Val Ala Glu Leu Val
5 10

25 (2) INFORMATION FOR SEQUENCE ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acid residues
(B) TYPE: amino acid
30 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

35 Ala Leu Val Glu Thr Ser Tyr Val Lys Val
5 10

(2) INFORMATION FOR SEQUENCE ID NO: 58:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acid residues

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- 5 (B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

10 Ser Thr Leu Val Glu Val Thr Leu Gly Glu Val
1 5 10

- 15 (2) INFORMATION FOR SEQUENCE ID NO: 59:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
20 (ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Leu Val Glu Val Thr Leu Gly Glu Val
1 5

25

- (2) INFORMATION FOR SEQUENCE ID NO: 60:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
30 (ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

35

Lys Met Val Glu Leu Val His Phe Leu
1 5

40

- (2) INFORMATION FOR SEQUENCE ID NO: 61:

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- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Val Ile Phe Ser Lys Ala Ser Glu Tyr Leu
1 5 10

- 15
(2) INFORMATION FOR SEQUENCE ID NO: 62:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acid residues
20 (B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

25 Tyr Leu Gln Leu Val Phe Gly Ile Glu Val
1 5 10

- (2) INFORMATION FOR SEQUENCE ID NO: 63:
30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Gln Leu Val Phe Gly Ile Glu Val Val
1 5

- 40 (2) INFORMATION FOR SEQUENCE ID NO: 64:
(i) SEQUENCE CHARACTERISTICS:

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- 5 (A) LENGTH: 11 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

10

Gln Leu Val Phe Gly Ile Glu Val Val Glu Val
1 5 10

15

- (2) INFORMATION FOR SEQUENCE ID NO: 65:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

20

Ile Ile Val Leu Ala Ile Ile Ala Ile
1 5

25

- (2) INFORMATION FOR SEQUENCE ID NO: 66:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acid residues
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

30

35

Lys Ile Trp Glu Glu Leu Ser Met Leu Glu Val
1 5 10

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5 (2) INFORMATION FOR SEQUENCE ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acid residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Ala Leu Ile Glu Thr Ser Tyr Val Lys Val

1

5

10

15

(2) INFORMATION FOR SEQUENCE ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acid residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

25

Leu Ile Glu Thr Ser Tyr Val Lys Val Leu

1

5

10

30

(2) INFORMATION FOR SEQUENCE ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acids

(D) TOPOLOGY linear

35

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: M3-195.203 OR SEQ ID NO: 69:

Ile Met Pro Lys Ala Gly Leu Leu Ile

40

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(2) INFORMATION FOR SEQUENCE ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acids

10

(D) TOPOLOGY linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: M3-220.228 OR SEQ ID NO: 70:

Lys Ile Trp Glu Glu Leu Ser Val Leu

15

5

(2) INFORMATION FOR SEQUENCE ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 14 amino acid residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

25

Ile Asn Phe Thr Arg Gln Arg Gln Pro Ser Glu Gly Ser Ser

5

10

30

(2) INFORMATION FOR SEQUENCE ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acid residues

(B) TYPE: amino acid

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Leu Phe Arg Ala Val Ile Thr Lys Lys Val Ala Asp

40

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10

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15 5 10

(2) INFORMATION FOR SEQ ID NO: 74

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1896 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

CGCGCGGTGG	CGGAGGCGGA	CACATTGGCG	TGAGACCTGG	GAGTACGTTG	TGCCAAATCA	60
TTGCCACTTG	CCACATGAGT	GTAAATGATG	GCGGATGCAA	GTATGTCTC	TGCCGATGGG	120
AAAAGCGATT	ATGGCCTGCG	AAGGTGACAG	CCATTATTCT	GTAACCTCAG	GACTTAGAAA	180
TGACTTTCGG	GTGACAAGTA	AAATCTTGAT	CAGGAGATAC	CTAGGATTTG	CTTCAGTGAA	240
ATAATTGAGC	CAGAACACGG	TTGGCACTGA	TTCTCGTTCC	CCATTTAATG	GGGTTTTGGT	300
CTAGTGCTTC	CAAGGTTACA	CTTCCAGAAA	TGTCTTTTTT	TTTTCACACT	AAAAAAAAAA	360
AAAAGAATCA	GCTGTAAAAA	GGCATGTAAG	GCTGTAACTC	AAGGAAAGAT	CTGGCAAGCA	420
GCCCTGTGAT	AGTAAATTAT	GGTCGTGTTT	AGGGAATGCT	TTCCAGCAAT	TCAGTAGACA	480
GTGCTCAGCT	GCAATGCAAA	AGCCCAGGTC	CTTGTCTTTG	TCTGCCACTG	GCCTCTCATG	540
CCTCAGTTTC	CCCATCTGTG	AAACAATGGG	GATTGGACCA	AATATCTGAA	ATCCCATGGT	600
TATAGGCCTT	CAGGATTACC	TGCTGCATTT	GTGCTAAAGT	TTGCCACTGT	TTCTCACTGT	660
CAGCTGTTGT	AATAACAAGG	ATTTTCTTTT	GTTTTAAATG	TAGGTTTTGG	CCCGAACCGC	720
GACTTCAACA	AAAAATAAGA	GAAGAAAGGA	ATATTTTCTA	GCTGTGCAAA	TCCTCTCCCT	780
AGAGGAAAAAG	TTAATTGTTG	TGTTGTTTTA	ATACTGTTTT	TTCCCGTGTA	GATTTCTGAT	840
ACTTCAATCC	CCTACTCCCC	CAAAACAGTT	GAAGCCCAGC	CCACTCTTAA	TGGGCTTATT	900

80

5 CACCATTTGT GTAATTCATT AATGCTCATA ATAACCTCAT GAGAAAGCAA CTAGTTTGAT 960
 TTTATGTCAG TTTGGAAGCT GAAGATCCAA ACGAGGCATT CTGTGAGATC TATGGAGAGA 1020
 TTGGTACAAA CACTGAATAC ATGTAAATTA TACTCAGGGT AGACCCTATT TGTGGTTAAA 1080
 ATAGGGATAT TTCCTTTTTT TTTTTTTTTT TTTGACTGT TTCTTAATCA GTGCCATGCC 1140
 AGGAAAATAG GGATGTTTCC TTCCCAGAGA TCTGTGTGTC TTTTTCAGA AACGTCTGTG 1200
 10 ACAGGCCCAT CAATTTTGAA ATATTTGGTT TTTGAGCCTG TCACTCTAAA CCAGCGTTTA 1260
 ACGTTCAAAA GGCAAATAAC TGATGACCAG GCGGCACATT GTTCTGCTCC GTGAGTGTCT 1320
 GGCAC TGGGA AAGGTGTAGA TTGTCTAGAA TGACAGCAAT TCCGACGCC CAGTCAGTCC 1380
 TCGTGATTG TGGCGAGGGC GCGTCTGGCA CCGGGAAGGT GTAGATCATC TAGAATGACG 1440
 GCGATTCCGA CGCCCCGGTC AGTCCTGCGT GATTGGCGAG GGTGCATCTG TCGTGAGAAT 1500
 15 TCCCAGTTCT GAAGAGAGCA AGGAGACTGA TCCCGCGTAG TCCAAGGCAT TGGCTCCCCT 1560
 GTTGCTCTTC CTTGTGGAGC TCCCCCTGCC CCACTCCCTC CTGCCTGCAT CTTCAGAGCT 1620
 GCCTCTGAAG CTCGCTTGGT CCCTAGCTCA CACTTTCCCT GCGGCTGGGA AGGTAATTGA 1680
 ATACTCGAGT TTAAGGAA AGCACATCCT TTAAACCAA AACACACCTG CTGGGCTGTA 1740
 AACAGCTTTT AGTGACATTA CCATCTACTC TGAATCTA ACAAAGGAGT GATTTGTGCA 1800
 20 GTTGAAAGTA GGATTTGCTT CATAAAGTC ACAATTTGAA TTCATTTTGT CTTTAAATC 1860
 CAGCCAACCT TTTCTGTCTT AAAAGGAAAA AAAAAA 1896

- 25 (2) INFORMATION FOR SEQUENCE ID NO: 75:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acid residues
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Glu Glu Lys Leu Ile Val Val Leu Phe

5

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- (2) INFORMATION FOR SEQUENCE ID NO: 76:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1554 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

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- 5 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: nucleic acid
- (ix) FEATURE:
- (A) NAME/KEY: DAGE
- (D) OTHER INFORMATION: Xaa is Arg when V is C or A or Gly
- 10 when V is G
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

15	VGA CTG AGA CCT AGA AAT CCA AGC GTT GGA GGT CCT GAG GCC AGC CTA	48
	Xaa Leu Arg Pro Arg Asn Pro Ser Val Gly Gly Pro Glu Ala Ser Leu	
	1 5 10 15	
20	AGT TTC CGC AAA ATG GAA CGA AGG CGT TTG CGG GGT TCC ATT CAG AGC	96
	Ser Arg Phe Lys Met Glu Arg Arg Arg Leu Arg Gly Ser Ile Gln Ser	
	20 25 30	
25	CGA TAC ATC AGC ATG AGT GTG TGG ACA AGC CCA CGG AGA CTT GTG GAG	144
	Arg Tyr Ile Ser Met Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu	
	35 40 45	
30	CTG GCA GGG CAG AGC CTG CTG AAG GAT GAG GCC CTG GCC ATT GCC GCC	192
	Leu Ala Gly Gln Ser Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala	
	50 55 60	
35	CTG GAG TTG CTG CCC AGG GAG CTC TTC CCG CCA CTC TTC ATG GCA GCC	240
	Leu Glu Leu Leu Pro Arg Glu Leu Phe Pro Pro Leu Phe Met Ala Ala	
	65 70 75 80	
40	TTT GAC GGG AGA CAC AGC CAG ACC CTG AAG GCA ATG GTG CAG GCC TGG	288
	Phe Asp Gly Arg His Ser Gln Thr Leu Lys Ala Met Val Gln Ala Trp	
	85 90 95	
40	CCC TTC ACC TGC CTC CCT CTG GGA GTG CTG ATG AAG GGA CAA CAT CTT	336
	Pro Phe Thr Cys Leu Pro Leu Gly Val Leu Met Lys Gly Gln His Leu	
	100 105 110	

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5	CAC CTG GAG ACC TTC AAA GCT GTG CTT GAT GGA CTT GAT GTG CTC CTT	384
	His Leu Glu Thr Phe Lys Ala Val Leu Asp Gly Leu Asp Val Leu Leu	
	115 120 125	
10	GCC CAG GAG GTT CGC CCC AGG AGG TGG AAA CTT CAA GTG CTG GAT TTA	432
	Ala Gln Glu Val Arg Pro Arg Arg Trp Lys Leu Gln Val Leu Asp Leu	
	130 135 140	
15	CGG AAG AAC TCT CAT CAG GAC TTC TGG ACT GTA TGG TCT GGA AAC AGG	480
	Arg Lys Asn Ser His Gln Asp Phe Trp Thr Val Trp Ser Gly Asn Arg	
	145 150 155 160	
20	GCC AGT CTG TAC TCA TTT CCA GAG CCA GAA GCA GCT CAG CCC ATG ACA	528
	Ala Ser Leu Tyr Ser Phe Pro Glu Pro Glu Ala Ala Gln Pro Met Thr	
	165 170 175	
25	AAG AAG CGA AAA GTA GAT GGT TTG AGC ACA GAG GCA GAG CAG CCC TTC	576
	Lys Lys Arg Lys Val Asp Gly Leu Ser Thr Glu Ala Glu Gln Pro Phe	
	180 185 190	
30	ATT CCA GTA GAG GTG CTC GTA GAC CTG TTC CTC AAG GAA GGT GCC TGT	624
	Ile Pro Val Glu Val Leu Val Asp Leu Phe Leu Lys Glu Gly Ala Cys	
	195 200 205	
35	GAT GAA TTG TTC TCC TAC CTC ATT GAG AGA GTG AAG CGA AAG AAA AAT	672
	Asp Glu Leu Phe Ser Tyr Leu Ile Glu Arg Val Lys Arg Lys Lys Asn	
	210 215 220	
40	GTA CTA CGG CTG TGC TGT AAG AAG CTG AAG ATT TTT GCA ATG CCC ATG	720
	Val Leu Arg Leu Cys Cys Lys Lys Leu Lys Ile Phe Ala Met Pro Met	
	225 230 235 240	
45	CAG GAT ATC AAG ATG ATC CTG AAA ATG GTG CAG CTG GAC TCT ATT GAA	768
	Gln Asp Ile Lys Met Ile Leu Lys Met Val Gln Leu Asp Ser Ile Glu	
	245 250 255	
50	GAT TTG GAA GTG ACT TGT ACC TGG AAG CTA CCC ACC TTG GCG AAA TTT	816

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5	Asp Leu Glu Val Thr Cys Thr Trp Lys Leu Pro Thr Leu Ala Lys Phe	
	260 265 270	
	TCT CCT TAC CTG GGC CAG ATG ATT AAT CTG CGT AGA CTC CTC CTC TCC	864
	Ser Pro Tyr Leu Gly Gln Met Ile Asn Leu Arg Arg Leu Leu Leu Ser	
10	275 280 285	
	CAC ATC CAT GCA TCT TCC TAC ATT TCC CCG GAG AAG GAA GAG AGT ATA	912
	His Ile His Ala Ser Ser Tyr Ile Ser Pro Glu Lys Glu Glu Ser Ile	
	290 295 300	
15	TCG CCC AGT TCA CCT CTC AGT TCC TCA GTC TGC AGT GCC TGC AGG CTC	960
	Ser Pro Ser Ser Pro Leu Ser Ser Ser Val Cys Ser Ala Cys Arg Leu	
	305 310 315 320	
20	TCT ATG TGG ACT CTT TAT TTT TCC TTA GAG GCC GCC TGG ACT CAG TTG	1008
	Ser Met Trp Thr Leu Tyr Phe Ser Leu Glu Ala Ala Trp Thr Gln Leu	
	325 330 335	
	CTC AGG CAC GTG ATG AAC CCC TTG GAA ACC CTC TCA ATA ACT AAC TGC	1056
25	Leu Arg His Val Met Asn Phe Leu Glu Thr Leu Ser Ile Thr Asn Cys	
	340 345 350	
	CGG CTT TCG GAA GGG GAT GTG ATG CAT CTG TCC CAG AGT CCC AGC GTC	1104
	Arg Leu Ser Glu Gly Asp Val Met His Leu Ser Gln Ser Pro Ser Val	
30	355 360 365	
	AGT CAG CTA AGT GTC CTG AGT CTA AGT GGG GTC ATG CTG ACC GAT GTA	1152
	Ser Gln Leu Ser Val Leu Ser Leu Ser Gly Val Met Leu Thr Asp Val	
	370 375 380	
35	AGT CCC GAG CCC CTC CAA GCT CTG CTG GAG AGA GCC TCT GCC ACC CTC	1200
	Ser Pro Glu Pro Leu Gln Ala Leu Leu Glu Arg Ala Ser Ala Thr Leu	
	385 390 395 400	
40	CAG GAC CTG GTC TTT GAT GAG TGT GGG ATC ACG GAT GAT CAG CTC CTT	1248
	Gln Asp Leu Val Phe Asp Glu Cys Gly Ile Thr Asp Asp Gln Leu Leu	

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5	405	410	415	
	GCC CTC CTG CCT TCC CTG AGC CAC TGC TCC CAG CTT ACA ACC TTA AGC			1296
	Ala Leu Leu Pro Ser Leu Ser His Cys Ser Gln Leu Thr Thr Leu Ser			
	420	425	430	
10	TTC TAC GGG AAT TCC ATC TCC ATA TCT GCC TTG CAG AGT CTC CTG CAG			1344
	Phe Tyr Gly Asn Ser Ile Ser Ile Ser Ala Leu Gln Ser Leu Leu Gln			
	435	440	445	
15	CAC CTC ATC GGG CTG AGC AAT CTG ACC CAC GTG CTG TAT CCT GTC CCC			1392
	His Leu Ile Gly Leu Ser Asn Leu Thr His Val Leu Tyr Pro Val Pro			
	450	455	460	
20	CTG GAG AGT TAT GAG GAC ATC CAT GGT ACC CTC CAC CTG GAG AGG CTT			1440
	Leu Glu Ser Tyr Glu Asp Ile His Gly Thr Leu His Leu Glu Arg Leu			
	465	470	475	480
25	GCC TAT CTG CAT GCC AGG CTC AGG GAG TTG CTG TGT GAG TTG GGG CGG			1488
	Ala Tyr Leu His Ala Arg Leu Arg Glu Leu Leu Cys Glu Leu Gly Arg			
	485	490	495	
30	CCC AGC ATG GTC TGG CTT AGT GCA ACC CCT GTC CTC ACT GTG GGG ACA			1536
	Pro Ser Met Val Trp Leu Ser Ala Thr Pro Val Leu Thr Val Gly Thr			
	500	505	510	
	GAA CCT TCT ATG ACC CGG			1554
	Glu Pro Ser Met Thr Arg			
	515			

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We claim:

1. Composition of matter comprising:
 - (i) a tumor rejection antigen precursor or a tumor rejection antigen, and at least one of:
 - (ii) a pharmaceutically acceptable adjuvant, and a T or B cell growth factor.
2. The composition of matter of claim 1, wherein said tumor rejection antigen precursor is a MAGE protein.
3. The composition of matter of claim 1, wherein said tumor rejection antigen precursor is a BAGE protein.
4. The composition of matter of claim 1, wherein said tumor rejection antigen precursor is a GAGE protein.
5. The composition of claim 1, wherein said tumor rejection antigen is derived from a MAGE protein.
6. The composition of matter of claim 5, wherein said MAGE protein is MAGE-1, MAGE-2, or MAGE-3.
7. The composition of matter of claim 6, wherein said tumor rejection antigen consists of one of SEQ ID NO: 1 through SEQ ID NO: 5.
8. The composition of matter of claim 1, wherein said pharmaceutically acceptable adjuvant is a substantially pure saponin derived from Quillaja saponaria.
9. The composition of matter of claim 8, wherein said substantially pure saponin is selected from the group consisting of QA-7, QA-21, QA-17, and QA-18.
10. The composition of matter of claim 1, wherein said pharmaceutically acceptable adjuvant is MTP-MF59.

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11. Method for stimulating an immune response in a subject comprising administering the composition of matter of claim 1 to said subject in an amount sufficient to provoke an immune response to said tumor rejection antigen precursor or tumor rejection antigen.

12. The method of claim 11, wherein said immune response comprises proliferation of T cells specific for complexes of said tumor rejection antigen and a major histocompatibility complex molecule to which said tumor rejection antigen binds.

13. The method of claim 11, wherein said T cells are cytolytic T cells.

14. The method of claim 11, wherein said immune response comprises production of antibodies against said tumor rejection antigen precursor or tumor rejection antigen.

15. The composition of claim 1, in intravenous form.

16. The composition of claim 1, in the form of a liposome.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/12463

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : A61K 38/00, 39/385, 45/00, 45/05; C07K 7/00, 14/00, 14/82

US CL : 424/185.1, 193.1, 277.1; 530/300, 350, 395, 868

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/185.1, 193.1, 277.1; 530/300, 350, 395, 868

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
Examiner's tumor rejection file referencesElectronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Automated Patent System and DIALOG (file = BIOCHEM). Key words: MAGE, tumor rejection antigen?

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US, A, 5,342,774 (BOON ET AL) 30 August 1994.	1-16
A, P	US, A, 5,405,940 (BOON ET AL.) 11 April 1995.	1-16
A, E	US, A, 5,462,871 (BOON-FALLEUR ET AL) 31 October 1995.	1-16
Y	R. W. Ellis (ed.) "Vaccines: New Approaches To Immunological Problems", published 1992 by Butterworth-Heinemann (Stoneham, MA), pages 431-449, see entire document.	1-16
Y	Vaccine, Volume 11, Issue 3, issued 1993, Gupta et al., "Adjuvants - a balance between toxicity and adjuvanticity", pages 293-306, see entire document.	1-16

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be part of particular relevance	*X*	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y*	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*G*	document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means		
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

03 JANUARY 1996

Date of mailing of the international search report

09 FEB 1996

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

THOMAS CUNNINGHAM

Telephone No. (703) 308-0196

International application No.
PCT/US95/12463

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Immunology Today, Volume 14, No. 6, issued 1993, Hadden; "Immunostimulants", pages 275-280, see entire document.	1-16